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FILE COVERS 1967 - 8 May 1996 (960508/ED) VOL 124 ISS 20

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Thesauri are now available for the WIPO International Patent Classifications (IPC) editions 1-6 in the /IC1, /IC2, /IC3, /IC4, /IC5, and /IC (/IC6) fields, respectively. The thesauri in the /IC5 and /IC fields also include the corresponding catchword terms from the IPC subject headings and subheadings.

- L1 40 SEA FILE=REGISTRY GAAGTTCCTATTC/SQSN
 L2 34 SEA FILE=REGISTRY GTATAGGAACTTC/SQSN
 L3 29 SEA FILE=REGISTRY L1(L)L2
 L4 5 SEA FILE=HCA L3
- L4 ANSWER 1 OF 5 HCA COPYRIGHT 1996 ACS
- AN 123:331869 HCA
- TI The role of DNA bending in Flp-mediated site-specific recombination
- AU Luetke, Karen H.; Sadowski, Paul D.
- CS Dep. Molecular and Medical Genetics, Univ. Toronto, Toronto, ON, M5S 1A8, Can.
- SO J. Mol. Biol. (1995), 251(4), 493-506 CODEN: JMOBAK; ISSN: 0022-2836
- DT Journal
- LA English
- L4 ANSWER 2 OF 5 HCA COPYRIGHT 1996 ACS
- AN 121:126321 HCA
- TI In vivo excision and amplification of large segments of the Escherichia coli genome
- AU Posfai, Gyorgy; Koob, Michael; Hradecna, Zdenka; Hasan, Noaman; Filutowicz, Marcin; Szybalski, Waclaw
- CS McArdle Lab. Cancer Res., Univ. Wisconsin, Madison, WI, 53706, USA
- SO Nucleic Acids Res. (1994), 22(12), 2392-8 CODEN: NARHAD; ISSN: 0305-1048
- DT Journal
- LA English
- L4 ANSWER 3 OF 5 HCA COPYRIGHT 1996 ACS
- AN 119:198292 HCA
- TI Ligation of synthetic activated DNA substrates by site-specific recombinases and topoisomerase I

- AN Guohua; Luetke, Karen; Juby, Carl D.; Brousseau, Roland; Sadowski, Paul
- CS Dep. Mol. Med. Genet., Univ. Toronto, Toronto, ON, M5S 1A8, Can.
- SO J. Biol. Chem. (1993), 268(5), 3683-9 CODEN: JBCHA3; ISSN: 0021-9258
- DT Journal
- LA English
- L4 ANSWER 4 OF 5 HCA COPYRIGHT 1996 ACS
- AN 114:1432 HCA
- TI Nucleotide sequence of a gene which enhances the activity of glyoxalase I in Saccharomyces cerevisiae
- AU Inoue, Yoshiharu; Feng, Ling; Bong-Young, Choi; Ginya, Harumi; Murata, Kousaka; Kimura, Akira
- CS Res. Inst. Food Sci., Kyoto Univ., Uji, 611, Japan
- SO Biotechnol. Appl. Biochem. (1990), 12(3), 341-5 CODEN: BABIEC; ISSN: 0885-4513
- DT Journal
- LA English
- L4 ANSWER 5 OF 5 HCA COPYRIGHT 1996 ACS
- AN 94:12618 HCA
- TI Nucleotide sequence of the yeast plasmid
- AU Hartley, James L.; Donelson, John E.
- CS Dep. Biochem., Univ. Iowa, Iowa City, IA, 52242, USA
- SO Nature (London) (1980), 286(5776), 860-5 CODEN: NATUAS; ISSN: 0028-0836
- DT Journal
- LA English

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn

Tue May 14 11:40:28 1996; MasPar time 2.46 Seconds 254.769 Million cell updates/sec Run on:

Tabular output not generated.

(1-34) from frt.seq 26 Description:

1 qaaqttcctattcNNNNNNNNqtataggaacttc 34 Perfect Score: N.A. Sequence:

cttcaaggataagNNNNNNNNcatatccttgaag Comp:

TABLE default Gap 10 Scoring table:

Dbase 0; Query 0 STD Nmatch 30947 seqs, 9219370 bases x 2 Searched:

Minimum Match 0% Post-processing:

Listing first 45 summaries

n-issued 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 10:PCT94 11:PCT95 Database:

Mean 5.064; Variance 2.619; scale 1.934 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	4.35e-08	4.35e-08	4.35e-08	2.38e-05	2.38e-05	2.38e-05	2.71e+00	2.71e+00	1.01e+01	1.0le+01
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Description	Sequence		Sequence							
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Query Match Length DB	34	89	7859	34	89	7859	1947	1997	1065	1689
Query Match	100.0	100.0	100.0	84.6	84.6	84.6	53.8	53.8	50.0	50.0
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US-07-998-	US-08-463-	PCT-US92-1	PCT-US95-0	US-07-750-	US-07-882-	PCT-US95-0	PCT-US93-0	PCT-US94-1	PCT-US94-1	PCT-US93-0	PCT-US93-0	US-07-753-	US-07-991~	us-07-753-	US-08-278-	PCT-US93-1	us-08-056-	PCT-US94-0	US-08-133-	US-08-277-	US-08-217-	PCT-US95-0	US-08-105-	PCT-US91-0	PCT-US93-0	PCT-US95-0	PCT-US95-0	PCT-US92-1	US-08-278-	PCT-US92-0	US-07-872	PCT-US95-0	US-08-045	PCT-US93-0	
		1947 8	1947 11	1988 4	2188 3			7493 10	7		7653 9	8316 3			31 4	237 9		1229 10		1749 4		-	2356 4		2757 9					4131 8		4146 11	5261 3	8538 9	
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ALI GNMENTS

MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL E Sequence 3, Application PC/TUS9201899.
Sequence 3, Application PC/TUS9201899
Sequence 1 Application PC/TUS9201899
Sequence 1 Application PC/TUS9201899
SEGUENCAL INFORMATION: FIFPHEN V.
TITLE OF INVENTION: FIFPHEN V.
TITLE OF INVENTION: HARMALIAN CELLS, AND COMPOSITIONS AND TITLE OF INVENTION: THEREFOR NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 В. PCT-US92-01899-3 STANDARD; DNA; UNC; 34 USA ర COUNTRY: STATE: 01-JAN-1900 XXXXXX RESULT

APPLICANT: WAHL, DR., GEOFFREY M.
APPLICANT: O'GORMAN DR., STEPHEN V.
ITILE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
TITLE OF INVENTION: MEMMALLIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
TITLE OF INVENTION: THEREFOR ö Gaps ö 8; Indels 100.0%; Score 26; DB 8; Length 34; 76.5%; Pred. No. 4.35e-08; NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000 INDIVIDUAL ISOLATE: FLP recombination target site COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other; 0; Mismatches 1 gaagttcctattcNNNNNNNNgtataggaacttc 34 1 GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC 34 PCT-US92-01899-4 STANDARD; DNA; UNC; 68 BP REFERENCE DOCKET NUMBER: P31 8929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown APPLICATION NUMBER: PCT/US92/01899 APPLICATION NUMBER: PCT/US92/01899 FILING DATE: 19920306 CLASSIFICATION: 800
ITTORNEY/AGENT INFORMATION:
NAME: REITER MR., STEPHEN E.
REIGSTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8929 Sequence 4, Application PC/TUS9201899. Sequence 4, Application PC/TUS9201899 GENERAL INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CURRENT APPLICATION DATA: 19920306 Best Local Similarity 76.5%; 26; Conservative CLASSIFICATION: 800 TOPOLOGY: unknown CDNA CITY: Los Angeles STATE: CA ORIGINAL SOURCE: COUNTRY: USA FILING DATE: MOLECULE TYPE: ZIP: 90071 01-JAN-1900 Query Match XXXXX Matches 88888888888888888888888888888888 숌 ð

TELECOMMUNICATION INFORMATION:

Gaps ·, 8; Indels Score 26; DB 8; Length 68; Pred. No. 4.35e-08; SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: ORIGINAL SOURCE: INDIVIDUAL ISOLATE: Synthetic oligonucleotide Sequence 68 BP; 19 A; 16 C; 14 G; 19 T; 0 other; APPLICANT: Czaplewski, Lloyd G TITLE OF INVENTION: Proteins and nucleic acids STREET: Ten South Wacker Drive, Suite 3000 0; Mismatches US-07-854-596B-4 STANDARD; DNA; UNC; 7859 BP 34 GAAGTTCCTATTCTCTAGAAGTATAGGAACTTC 67 1 gaagttcctattcNNNNNNNNgtataggaacttc 34 APPLICATION NUMBER: US/07/854,596B FILING DATE: 03-JUN-1992 ADDRESSEE: Dr. John J. McDonnell COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 4, Application US/07854596B. Sequence 4, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION: REGISTRATION NUMBER: 26,949 APPLICANT: Dawson, Keith M APPLICANT: Hunter, Michael G REFERENCE/DOCKET NUMBER: 9; TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000 TELEFAX: 312-715-1234 TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: TELEX: 910-221-5317 INFORMATION FOR SEQ ID NO: 4: (619) 535-9001 ATTORNEY/AGENT INFORMATION: LENGTH: 7859 base pairs NAME: McDonnell, John J LENGTH: 68 base pairs STRANDEDNESS: unknown Query Match 100.0%; Best Local Similarity 76.5%; Matches 26; Conservative NUMBER OF SEQUENCES: 73 SEQUENCE CHARACTERISTICS CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 TYPE: NUCLEIC ACID nucleic acid TOPOLOGY: unknown MOLECULE TYPE: cDNA Chicago COUNTRY: USA ZIP: 60606 TELEPHONE: STATE: IL 01-JAN-1900 XXXXXX RESULT ID US AC xx 염 888888888888888 ð

STRANDEDNESS: single

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34 GAAGTICCTAITCTCTAGAAAGTAIAGGAACTIC 67 34 gaagttcctatacNNNNNNNNgaataggaacttc 1 XXXXXX Matches 쉱 გ 쇰 გ APPLICANT: WAIL, DR., GEOFFREY M.
APPLICANT: O'GORMAN DR., STEPHEN V.
TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL.
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4 ö Gaps ö OTHER INFORMATION: /note= "sequence of plasmid pSW6" Sequence 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other; Query Match 100.0%; Score 26; DB 4; Length 7859; Best Local Similarity 76.5%; Pred. No. 4.35e-08; Matches 26; Conservative 0; Mismatches 8; Indels CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000 INDIVIDUAL ISOLATE: FLP recombination target site Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other; CONDUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US92/01899
FILING DATE: 19920306
CLASSIFICATION: 800 3131 GAAGTTCCTATTCTCTAGAAGTATAGGAACTTC 3164 JT 4 PCT-US92-01899-3 STANDARD; DNA; UNC; 34 BP. REFERENCE/DOCKET NUMBER: P31 8929 TELECOMMUNICATION: Sequence 3, Application PC/TUS9201899. Sequence 3, Application PC/TUS9201899 ATTORNEY/AGENT INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 INFORMATION FOR SEQ ID NO: 3: TELEPHONE: (619) 535-9001 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk (619) 535-8949 NAME/KEY: misc feature LOCATION: 1..7859 SEQUENCE CHARACTERISTICS: LENGTH: 34 base pairs STRANDEDNESS: unknown TOPOLOGY: circular TYPE: NUCLEIC ACID MOLECULE TYPE: CDNA ORIGINAL SOURCE: MOLECULE TYPE: CDNA TOPOLOGY: unknown CITY: Los Angeles GENERAL INFORMATION: USA ZIP: 90071 STATE: CA COUNTRY: TELEFAX: 01-JAN-1900 FEATURE: Query Match XXXXXX RESULT 88888888 ਨ

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APPLICANT: WAHL, DR., GEOFFREY M.
APPLICANT: O'GORMAN DR., STEPHEN V.
TITLE OF INVENTION: FLA-MEDIATED GENE MODIFICATION IN
TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ö ö Gaps Gaps ö ö 0; Mismatches 10; Indels 84.6%; Score 22; DB 8; Length 68; 70.6%; Pred. No. 2.38e-05; 0; Mismatches 10; Indels Score 22; DB 8; Length 34; Pred. No. 2.38e-05; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000 SOFTWARE: PatentIn Release #1.0, Version #1.25 INDIVIDUAL ISOLATE: Synthetic oligonucleotide Sequence 68 BP; 19 A; 16 C; 14 G; 19 T; 0 other; LT 5 PCT-US92-01899-4 STANDARD; DNA; UNC; 68 BP 1 GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC 34 34 gaagttcctatacNNNNNNNNNgaataggaacttc 1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01899
FILING DATE: 19920306 = = = = = REFERENCE/DOCKET NUMBER: P31 8929 Sequence 4, Application PC/TUS9201899. Sequence 4, Application PC/TUS9201899 GENERAL INFORMATION: OPERATING SYSTEM: PC-DOS/MS-DOS CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 COMPUTER: IBM PC compatible TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: TELEPHONE: (619) 535-9001 MEDIUM TYPE: Floppy disk TELEFAX: (619) 535-8949 STRANDEDNESS: unknown Query Match
Best Local Similarity 70.6%; Query Match 84.6%; Best Local Similarity 70.6%; LENGTH: 68 base pairs COMPUTER READABLE FORM: 24; Conservative TYPE: NUCLEIC ACID CDNA Los Angeles TOPOLOGY: unknown ORIGINAL SOURCE: USA MOLECULE TYPE: ZIP: 90071 STATE: CA COUNTRY: 01-JAN-1900

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DT UL-JAM-1900 DE Sequence 4, Application PC/TUS9301720. CC Sequence 4, Application PC/TUS9301720. CC GENERAL INFORMATION: CC APPLICANT: Renauld, Jean-Christophe CC APPLICANT: Van Shick, Jacques CC APPLICANT: Van Shick, Jacques CC TITLE OF INVENTION: Nucleic Acid Sequences Coding For CC TITLE OF INVENTION: Or Complementary To Nucleic Acid Sequences Coding	CC NUMBER OF SEQUENCES: 6 CC NUMBER OF SEQUENCES: 6 CC CORRESPONDENCE ADDRESS: CC ADDRESSEE: Felfe & Lynch CC STREET: 805 Third Avenue CC CITY: New York City CC STATE: New York CC COUNTRY: USA CC COUNTRY: USA CC COUNTRY: USA CC CONPUTER READBLE FORM: CC COMPUTER: IBM PS/2 CC COMPUTER:	PR AT TE INFC SE Seque	y Ma Loc hes 121 28	HESULI 8 ID PUT-0893-01720-6 STANDARD; DNA; UNC; 1997 BP AC XXXXXX DT 01-JAN-1900 DE Sequence 6, Application PC/TUS9301720 CC Sequence 6, Application PC/TUS9301720 CC GENERAL INFORMATION: CC APPLICANT: Renauld, Jean-Christophe CC APPLICANT: Druez, Catherine
SULT SULT S	CC GENERAL INFORMATION: CC APPLICANT: Dawson, Keith M CC APPLICANT: Hunter, Michael G CC APPLICANT: Hunter, Michael G CC APPLICANT: Czaplewski, Lloyd G CC TITLE OF INVENTION: Proteins and nucleic acids CC TITLE OF INVENTION: Proteins and nucleic acids CC CORRESPONDENCE ADDRESS: CC CORRESPONDENCE ADDRESS: CC CORRESPONDENCE ADDRESS: CC COUNTRY: Us A CC STREET: Ten South Wacker Drive, Suite 3000 CC STREET: LL CC COUNTRY: UsA CC COUNTRY: UsA CC COUNTRY: USA CC COMPUTER READABLE FORM: CC COMPUTER READABLE FORM: CC COMPUTER READABLE FORM: CC COMPUTER: IBM PC compatible CC COMPUTER: BM PC compatible CC COMPUTER: Datentl Nelease #1.0, Version #1.25	IN	CC MOLECULE TYPE: CDNA CC FEATURE: CC NAME/KEY: misc_feature CC LOCATION: 17859 CC OTHER INFORMATION: /note= "sequence of plasmid pSW6" SQ Sequence 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other; Query Match 84.6%; Score 22; DB 4; Length 7859; Best Local Similarity 70.6%; Pred. No. 2.38e-05; Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	Db 3131 GAACTTCCTATTCTCTAGAAGTATAGGAACTTC 3164

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g გ APPLICANT: Van Snick, Jacques TITLE OF INVENTION: Nucleic Acid Sequences Coding For TITLE OF INVENTION: Or Complementary To Nucleic Acid Sequences Coding ö Gaps APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation ö Query Match 53.8%; Score 14; DB 9; Length 1997; Best Local Similarity 60.7%; Pred. No. 2.71e+00; COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01720
FILING DATE: 19930225 0; Mismatches 11; Indels Sequence 1997 BP; 388 A; 612 C; 593 G; 404 T; 0 other; TITLE OF INVENTION: Interleukin 9 Receptor US-08-292-549-5 STANDARD; DNA; UNC; 1065 BP. NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688–9200
TELEFAX: (212) 838–9884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US/07/847,347 1171 CCTCTACAGTGTACACAATGGGAACTTC 1198 28 cctatacNNNNNNNNgaataggaacttc 1 Sequence 5, Application US/08292549.
Sequence 5, Application US/08292549
Patent No. 5464938
GENERAL INFORMATION: STREET: 51 University Street = = = = FILING DATE: 09-MARCH-1992 ATTORNEY/AGENT INFORMATION: ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue LENGTH: 1997 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: 17; Conservative CITY: New York City NUMBER OF SEQUENCES: TOPOLOGY: linear STATE: New York CLASSIFICATION: COUNTRY: USA ZIP: 10022 01-JAN-1900 XXXXXX Matches RESULT

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Seattle

ö Partent No. 54/6781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 54/6781el Entomopoxvirus Expression System NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik Gaps ö Score 13; DB 4; Length 1065; Pred. No. 1.01e+01; 0; Mismatches 10; Indels Sequence 1065 BP; 327 A; 248 C; 197 G; 293 T; 0 other; SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: STREET: 2421 N.W. 41st Street, Suite A-1 US-07-991-867B-41 STANDARD; DNA; UNC; 1689 BP. APPLICATION NUMBER: US/08/292,549 FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,330
FILING DATE: 10/19/92
ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2602-A Sequence 41, Application US/07991867B. Sequence 41, Application US/07991867B OPERATING SYSTEM: PC-DOS/MS-DOS 384 TTCCCAAACAAGTGTGGAATAGGA 408 COMPUTER: IBM PC compatible TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430 TELEFAX: (206) 233-0644 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1065 base pairs 30 ttcctatacNNNNNNNNgaatagga 6 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO MEDIUM TYPE: Floppy disk ORGANISM: Cowpox virus Query Match 50.0%; Best Local Similarity 60.0%; STRANDEDNESS: single COMPUTER READABLE FORM: 15; Conservative TYPE: nucleic acid Washington LOCATION: 1..1065 TOPOLOGY: linear NAME/KEY: CDS ORIGINAL SOURCE: COUNTRY: USA ANTI-SENSE: NO 98101 01-JAN-1900 RESULT 10 XXXXXX Matches

Sequence 2, Application US/0798972A.
Sequence 2, Application US/0798972A.
Sequence 2, Application US/0798972A.
Patent No. 5476777
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower, US-07-998-972A-2 STANDARD; DNA; UNC; 1947 BP 01-JAN-1900 RESULT 111 US-07-5 US-

May 14 11:31

ö Gaps ; 0 Score 13; DB 4; Length 1947; Pred. No. 1.01e+01; 0; Mismatches 12; Indels Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.25 REFERENCE/DOCKET NUMBER: 13952-12-2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A APPLICATION NUMBER: US 07/816, 281 FILING DATE: 31-DEC-1991 ATTORNEY/AGENT INFORMATION: 1204 TCCTGTACCCGCCTGGGACAGAACTTC 1232 FILING DATE: 19921230 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/860,701 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS 29 tcctatacNNNNNNNNgaataggaacttc 1 REGISTRATION NUMBER: 31,990 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS: FILING DATE: 31-MAR-1992 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NAME: Parmelee, Steven W LENGTH: 1947 base pairs ORGANISM: Homo sapiens Query Match 50.0%; Best Local Similarity 58.6%; TYPE: nucleic acid STRANDEDNESS: single TISSUE TYPE: Hepatic 17; Conservative 3..1847 TOPOLOGY: linear NAME/KEY: CDS ORIGINAL SOURCE: 94105 LOCATION: Matches g

Sequence 2, Application US/08463953.
Sequence 2, Application US/08463953.
Sequence 2, Application US/08463953.
Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS: US-08-463-953-2 STANDARD; DNA; UNC; 1947 BP. 01-JAN-1900 XXXXXX RESULT 12

STREET: One Market Plaza, Stewart Street Tower,

Twentieth Floor

STREET:

San Francisco

ADDRESSEE: Townsend and Townsend

ö Gaps ö Query Match 50.0%; Score 13; DB 5; Length 1947; Best Local Similarity 58.6%; Pred. No. 1.01e+01; Antches 17; Conservative 0; Mismatches 12; Indels APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48 LOCATION: 3.1847 Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower, COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 PCT-US92-11357-2 STANDARD; DNA; UNC; 1947 BP. CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 13952-12-2 TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953 1204 TCCTGTACCCGCCCTGGGACAAGAACTTC 1232 Sequence 2, Application PC/TUS9211357. Sequence 2, Application PC/TUS9211357 GENERAL INFORMATION: 29 tcctatacNNNNNNNNNgaataggaacttc 1 = = --NAME: Parmelee, Steven W REGISTRATION NUMBER: 31,990 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1947 base pairs COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TELEPHONE: 206-467-9600 TELEFAX: 415-543-5043 Twentieth Floor ORIGINAL SOURCE: ORGANISM: Homo sapiens TYPE: nucleic acid STRANDEDNESS: single TISSUE TYPE: Repatic San Francisco TOPOLOGY: linear NAME/KEY: CDS USA FILING DATE: ZIP: 94105 STREET: 01-JAN-1900 g g,

CITY: San Francisco

Gaps ö BOARD OF REGENTS, THE UNIVERSITY OF Score 13; DB 8; Length 1947; Pred. No. 1.01e+01; 0; Mismatches 12; Indels MEDIUM TREE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
FILING DATE: 19921230
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701 LOCATION: 3..1847 Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; COUNTRY: United States of America POSTAL CODE: 78701 PCT-US95-07439-24 STANDARD; DNA; UNC; 1947 BP 201 West 7th Street Sequence 24, Application PC/TUS9507439.
Sequence 24, Application PC/TUS9507439
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: BOARD OF REGENTS,
APPLICANT: TEXAS SYSTEM RECISTRATION NUMBER: 31,990 REFERENCE/DOCKET NUMBER: 13952-12-2 1204 TCCTGTACCCGCCCTGGGACAAGAACTTC 1232 APPLICATION NUMBER: US 07/816,281 FILING DATE: 31-DEC-1991 ATTORNEY/AGENT INFORMATION: 29 tcctatacNNNNNNNNNgaataggaacttc 1 TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1947 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single Austin FILING DATE: 31-MAR-1992 PRIOR APPLICATION DATA: NAME: Parmelee, Steven W ORGANISM: Homo sapiens Query Match 50.0%; Best Local Similarity 58.6%; 17; Conservative COMPUTER READABLE FORM: TISSUE TYPE: Hepatic STREET: TOPOLOGY: linear STATE: NAME/KEY: CDS LOCATION: 3..1 USA ORIGINAL SOURCE: 94105 APPLICANT: APPLICANT: COUNTRY: APPLICANT: APPLICANT: 01-JAN-1900 XXXXXX RESULT 14 Matches გ

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APPLICANT:

გ ö ; 0 Query Match 50.0%; Score 13; DB 11; Length 1947; Best Local Similarity 58.6%; Pred. No. 1.01e+01; 0; Mismatches 12; Indels THE SCRIPPS RESEARCH INSTITUTE 10666 North Torrey Pines Road Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; APPLICANT: POSTAL CODE: 92037 TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: FOR THE SPECIFIC TITLE OF INVENTION: COAGULATION OF VASCULATURE COUNTRY: United States of America US-07-750-080A-15 STANDARD; DNA; UNC; 1988 BP COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII CURRENT APPLICATION DATA: TELEPHONE NO: (512)499-4462 TELEFAX: (512)499-4523 NAME: PARKER, DAVID L. REGISTRATION NUMBER: 32,165 REFERENCE/DOCKET NUMBER: UTFD433P--APPLICATION NUMBER: PCT/US95/07439 FILING DATE: Concurrently herewith APPLICATION NUMBER: US 08/273,567 ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 1204 fccfgfacccgcccfggacaagaacffc 1232 Sequence 15, Application US/07750080A. Sequence 15, Application US/07750080A Patent No. 5445953 GENERAL INFORMATION: APPLICANT: DORNER, F. 29 tcctatacNNNNNNNNgaataggaacttc 1 California FELECOMMUNICATION INFORMATION: LaJolla INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679 FILING DATE: 11-JUN-1994 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk LENGTH: 1947 base pairs NUMBER OF SEQUENCES: 27 TYPE: nucleic acid STRANDEDNESS: single CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: 17; Conservative STREET: TOPOLOGY: linear CITY: STATE: TELEX: 79-0924 CLASSIFICATION: NAME: CITY: Houston STATE: Texas COUNTRY: USA ZIP: 77210 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: 01-JAN-1900 RESULT 15 XXXXXX Matches g გ

May 14 11:31 R.P.mi 1.2

Gaps Sequence 4, Application US/07882925A.
Sequence 4, Application US/07882925A
Patent No. 5315000
GENERAL INFORMATION:
APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its cDNA and FITLE OF INVENTION: protein TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED TITLE OF INVENTION: EUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME ö Query Match 50.0%; Score 13; DB 4; Length 1988; Best Local Similarity 58.6%; Pred. No. 1.01e+01; Matches 17; Conservative 0; Mismatches 12; Indels CLONE: palS1-PT (Fig. 5.1) Sequence 1988 BP; 451 A; 529 C; 617 G; 391 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: STREET: Wood, Herron & Evans, 2700 Carew Tower REFERENCE/DOCKET NUMBER: 30472/106 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELERX: (903) 833-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS: US-07-882-925A-4 STANDARD; DNA; UNC; 2188 BP STREET: 1800 Diagonal Road, Suite 500 APPLICATION NUMBER: US/07/750,080A FILING DATE: 19910826 COUNTRY: USA
Z1P: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 1247 TCCTGTACCCGCCTGGGACAAGAACTTC 1275 29 tcctatacNNNNNNNNgaataggaacttc 1 REGISTRATION NUMBER: 29,768 ADDRESSEE: Foley & Lardner MOLECULE TYPE: DNA (genomic) APPLICANT: SCHEIFLINGER, F. ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. ADDRESSEE: Gregory Lunn APPLICANT: FALKNER, F. G. LENGTH: 1988 base pairs NUMBER OF SEQUENCES: 42 TYPE: NUCLEIC ACID STRANDEDNESS: single NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 TOPOLOGY: linear CITY: Alexandria IMMEDIATE SOURCE: 01-JAN-1900 RESULT 16 XXXXXX

May 14 11.31 H.P.mi

Sequence 1, Application PC/TUS9305651.
Sequence 1, Application PC/TUS9305651
GENERAL INFORMATION:
ITILE OF INVENTION:
A Gene Which Prevents Programmed Cell Death
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette Gaps ö Score 13; DB 11; Length 2553; Pred. No. 1.01e+01; 0; Mismatches 12; Indels Sequence 2553 BP; 749 A; 535 C; 610 G; 659 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE FITLE OF INVENTION: CONTRACEPTIVE VACCINE RESULT 18 ID PCT-US93-05651-1 STANDARD; DNA; UNC; 6560 BP. CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6560 base pairs REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEPA: (908) 594-470
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2553 base pairs APPLICATION NUMBER: PCT/US95/07295 767 AAGTTGCTCTACAGGTTCCTGAAGTGGAA 795 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 33 aagttcctatacNNNNNNNgaataggaa 5 ADDRESSEE: MARY A. APPOLLINA ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A
REGISTRATION NUMBER: 34,087 Query Match 50.0%; Best Local Similarity 58.6%; TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double CORRESPONDENCE ADDRESS: 17; Conservative 17..2221 NUMBER OF SEQUENCES: MOLECULE TYPE: CDNA TOPOLOGY: linear CLASSIFICATION: NAME/KEY: CDS COUNTRY: USA ZIP: 07065 CITY: RAHWAY STATE: NJ FILING DATE: LOCATION: 01-JAN-1900 Matches XXXXXX გ

NAME/KEY: misc_feature

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Gaps ; 0 NAME/KEY: misc_feature LOCATION: 408.7367 OTHER INFORMATION: /product= "Coagulation Factor VIII" Score 13; DB 10; Length 7493; RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476 Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other; 0; Mismatches 11; Indels APPLICANT: Emory University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: AUTHORS: Lakich, D.
AUTHORS: Gitschier, J.
ITILE: Sequence of the Murine Factor VIII cDNA. OPPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: OTHER INFORMATION: /function= "PolyA_signal" Pred. No. 1.01e+01; ADDRESSEE: Kilpatrick & Cody STREET: 1100 Peachtree Street, Suite 2800 OTHER INFORMATION: /rpt_type="terminal" OTHER INFORMATION: /note="3'UTR" PCT-US94-13200-5 STANDARD; DNA; UNC; 7493 BP ATTORNEY/ACENT INFORMATION:
NAME: Pabst, Patrea L.
RECISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMUIO6CIP(2) APPLICATION NUMBER: PCT/US94/13200 3714 GAAGATCCTATTCCACAAGATGAAGAG 3740 Sequence 5, Application PC/TUS9413200. Sequence 5, Application PC/TUS9413200 COMPUTER: IBM PC compatible COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk FILING DATE: 15-NOV-1994 TELEPHONE: 404-815-6508 NAME/KEY: repeat unit LOCATION: 7368..7493 PUBLICATION INFORMATION: AUTHORS: Elder, F. Query Match 50.0%; Best Local Similarity 59.3%; 16; Conservative LOCATION: 7471..7476 JOURNAL: Genomics GENERAL INFORMATION: CITY: Atlanta STATE: Georgia CLASSIFICATION: 374-379 COUNTRY: US 1993 ZIP: 30309 AUTHORS: AUTHORS: VOLUME: PAGES: 01-JAN-1900 FEATURE: RESULT 20 XXXXXX Matches 셤 88888888888888888888888888888 3

ORIGINAL SOURCE: ANTI-SENSE: NO

TITLE OF INVENTION: Cloning and Characterization of Cell Death Genes NUMBER OF SEQUENCES: 29 Sequence 7653 BP; 2429 A; 1455 C; 1271 G; 2498 T; 0 other; Query Match 50.0%; Score 13; DB 9; Length 7653; Best Local Similarity 60.0%; Pred. No. 1.01e+01; MOLECULE TYPE: DNA (genomic) Sequence 7653 BP; 2429 A; 1455 C; 1271 G; 2498 T; 0 other; Query Match 50.0%; Score 13; DB 9; Length 7653; Best Local Similarity 60.0%; Pred. No. 1.01e+01; 0; Mismatches 10; Indels ADDRESSEE: Massachusetts Institute of Technology STREET: 77 Massachusetts Avenue APPLICANT: Massachusetts Institute of Technology LT 22 PCT-US93-05701-18 STANDARD; DNA; UNC; 7653 BP. APPLICATION NUMBER: PCT/US93/05705 APPLICATION NUMBER: PCT/US93/05701 Sequence 18, Application PC/TUS9305701 Sequence 18, Application PC/TUS9305701 GENERAL INFORMATION: 4399 TATTCCATGAAGAGGATATGAACTT 4423 9 tattcNNNNNNNNStataggaactt 33 MOLECULE TYPE: DNA (genomic) INFORMATION FOR SEQ ID NO: 18: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 7653 base pairs SEQUENCE CHARACTERISTICS: LENGTH: 7653 base pairs TYPE: nucleic acid STRANDEDNESS: double = = = = CURRENT APPLICATION DATA: CURRENT APPLICATION DATA: FILING DATE: 19930614 COMPUTER READABLE FORM: MEDIUM TYPE: diskette MEDIUM TYPE: diskette FILING DATE: 19930714 TYPE: nucleic acid STRANDEDNESS: double CITY: Cambridge STATE: Massachusetts CORRESPONDENCE ADDRESS: Massachusetts COMPUTER READABLE FORM: 15; Conservative OPERATING SYSTEM: linear TOPOLOGY: linear COUNTRY: U.S.A. COUNTRY: U.S.A. CLASSIFICATION: ZIP: 02139 ZIP: 02139 TOPOLOGY: COMPUTER: SOF TWARE: 01-JAN-1900 Matches a 888888888888888888888888888888888 ð ö Gaps Sequence 1, Application PC/TUS9305705.
Sequence 1, Application PC/TUS9305705
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Inhibitors of Ced-3 and Related Proteins
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Massachusetts Institute of Technology
STREET: 77 Massachusetts Avenue ö NAME/KEY: misc_feature
LOCATION: 408._7367
OTHER INFORMATION: /product= "Coagulation Factor VIII"
PUBLICATION INFORMATION: RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476 Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other; Query Match 50.0%; Score 13; DB 10; Length 7493; Best Local Similarity 59.3%; Pred. No. 1.01e+01; 0; Mismatches 11; Indels AUTHORS: Lakich, D. AUTHORS: Gitschier, J. IITLE: Sequence of the Murine Factor VIII CDNA. NAME/KEY: misc_feature LOCATION: 7471_.7476 OTHER INFORMATION: /function= "PolyA_signal" OTHER INFORMATION: /rpt_type="terminal" OTHER INFORMATION: /note= "5'UTR" OTHER INFORMATION: /rpt_type="terminal" OTHER INFORMATION: /note="3'UTR" PCT-US93-05705-1 STANDARD; DNA; UNC; 7653 BP. 3714 GAAGATCCTATTCCACAAGATGAAGAG 3740 34 gaagttcctatacNNNNNNNNgaatag 8 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 7493 base pairs TYPE: nucleic acid STRANDEDNESS: single MOLECULE TYPE: CDNA to mRNA ORGANISM: Mus musculus NAME/KEY: repeat_unit LOCATION: 7368..7493 NAME/KEY: repeat_unit LOCATION: 1..407 16; Conservative AUTHORS: Elder, F. Genomics TOPOLOGY: linear 374-379 HYPOTHETICAL: NO

VOLUME: 16

Matches

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AUTHORS: JOURNAL:

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ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Center, 1420 Fifth Avenue TELECOMMUNICATION INFORMATION: TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct) TELEFAX: 1-206-224-0779 GENERAL INFORMATION:

APPLICANT: Tapscott, J.; Weintraub, H.M.; Palmer, T.D.

TITLE OF INVENTION: "MyoD REGULATORY REGION"

NUMBER OF SEQUENCES: 4 MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01 SOFTWARE: Word for Windows-t CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,520B US-07-753-5208-4 STANDARD; DNA; UNC; 8316 BP. NAME: Sundsmo, John, S. REGISTRATION NUMBER: 34,446 REFERENCE/DOCKET NUMBER: FHCR-1-5789 Sequence 4, Application US/07753520B. Sequence 4, Application US/07753520B MOLECULE TYPE: Other; plasmid DNA TELEX: 4938023
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8316 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single APPLICATION NUMBER: none FILING DATE: none ATTORNEY/AGENT INFORMATION: FILING DATE: 19910903 PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: CLASSIFICATION: 435 CITY: Seattle STATE: Washington TOPOLOGY: linear ZIP: 98101-2347 Patent No. 5352595 COUNTRY: USA 01-JAN-1900 XXXXXX RESULT

TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIKG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: STREET: 2421 N.W. 41st Street, Suite A-1 ORGANISM: Amsacta moorei entomopoxvirus US-07-991-867B-1 STANDARD; DNA; UNC; 8457 BP APPLICATION NUMBER: US/07/991,867B REGISTRATION NUMBER: 31,794 REFERENCE/DOCKET NUMBER: UF114.C3 TELECOMMUNICATION INFORMATION: APPLICATION NUMBER: US 07/827, 685 FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA: Sequence 1, Application US/07991867B. Sequence 1, Application US/07991867B Patent No. 5476781 GENERAL INFORMATION:
APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E. APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: WO 92/14818 FILING DATE: 12-FEB-1992 ADDRESSEE: David R. Saliwanchik complement (65..1459) NAME: Saliwanchik, David R. MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 8457 base pairs FILING DATE: 12-DEC-1992 TELEPHONE: 904-375-8100 25 atacNNNNNNNNgaataggaa 5 TELEFAX: 904-372-5800 TYPE: nucleic acid STRANDEDNESS: double CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: CLASSIFICATION: 435 NUMBER OF SEQUENCES: CITY: Gainesville STATE: FL TOPOLOGY: unknown NAME/KEY: CDS COUNTRY: USA LOCATION: 01-JAN-1900 FEATURE: XXXXXX RESULT ç

NAME/KEY: CDS

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8; Indels

Mismatches

13; Conservative

Matches

Best Local Similarity

Query Match

Score 13; DB 3; Length 8316; Pred. No. 1.01e+01;

50.0%; 61.9%;

pLHDMDN-NSA: 5'LTR (position 1-1159); y+ (position 1160-1640); HisD (position 1641-2928), Myo-D NSA Apal f

DESCRIPTION: DESCRIPTION: DESCRIPTION: (position 2929-4389); driving neo (position 4390-5259);

DESCRIPTION: (position 5260-5964); Figures 8A-8C. Sequence 8316 BP; 1922 A; 2246 C; 2255 G; 1880 T; 13 other;

with 3'LTR

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MOLECULE TYPE: Other;plasmid DNA DESCRIPTION: pLHDMDN-53: 5'LTR (position 1-1159); Y+ (position DESCRIPTION: 1159-1640); HisD (position 1641-3007); Myo-D 531.4 Apal DESCRIPTION: (position 3008-5248); driving neo (position 5249-6117); DESCRIPTION: 3'LTR (position 6118-6823) coupled to a pBR322 plasmid APPLICANT: Thompson, Mark APPLICANT: Gaertner, Frank H. TITLE OF INVENTION: No. 5468483el Bacillus thuringiensis Isolate TITLE OF INVENTION: Having Anti-Protozoan Activity Gaps ö DESCRIPTION: 6824-9115); Figures 7A-7D. Sequence 9115 BP; 2183 A; 2408 C; 2474 G; 2036 T; 14 other; Query Match 50.0%; Score 13; DB 3; Length 9115; Best Local Similarity 61.9%; Pred. No. 1.01e+01; 8; Indels COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roman Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL 0; Mismatches US-08-278-685-4 STANDARD; DNA; UNC; 31 BP. APPLICATION NUMBER: US 07/654,166 FILING DATE: 12-FEB-1991 APPLICATION NUMBER: US/08/278, 685 Sequence 4, Application US/08278685. Sequence 4, Application US/08278685 Patent No. 5468483 GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk 241 ATACATAACTGAGAATAGGAA 261 LENGTH: 9115 base pairs 25 atacNNNNNNNNgaataggaa 5 TYPE: NUCLEIC ACID STRANDEDNESS: single PRIOR APPLICATION DATA: 13; Conservative CLASSIFICATION: 435 TOPOLOGY: linear COUNTRY: USA FILING DATE: ZIP: 32606 01-JAN-1900 XXXXXX fragment (position Matches with a RESULT ဗ පු ც 8888888 ပ္ပ

REGISTRATION NUMBER: 21,023 REFERENCE/DOCKET NUMBER: 07/654,166

NAME: Saliwanchik, Roman

ELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

APPLICATION NUMBER: US 08/091,527 FILING DATE: 12-AUG-1993 ATTORNEY/AGENT INFORMATION:

TELEFAX: 904-372-5800

LENGTH: 31 base pairs TYPE: nucleic acid STRANDEDNESS: single

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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) Sequence 31 BP; 6 A; 6 C; 10 G; 9 T; 0 other;

Gaps ö Query Match 46.2%; Score 12; DB 4; Length 31; Best Local Similarity 59.1%; Pred. No. 3.58e+01; Matches 13; Conservative 0; Mismatches 9; Indels 13; Conservative Matches

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7 GAACTTCCTATTCGTGGTG 28 용

1 gaagttcctattcNNNNNNNg 22

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PCT-US93-10443-9 STANDARD; DNA; UNC; 237 BP. XXXXXX

01-JAN-1900

Sequence 9, Application PC/TUS9310443.

APPLICANT: David D. Moore
APPLICANT: Jae W. Lee
TITLE OF INVEXTION: NUCLEAR HORMONE RECEPTORTITLE OF INVEXTION: RELATED MOLECULES AND
TITLE OF INVEXTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street

CITY: Boston STATE: Massachusetts

COUNTRY: U.S.A. ZIP: 02110-2804

COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10443 FILING DATE:

APPLICATION NUMBER: 07/969,136 PRIOR APPLICATION DATA: CLASSIFICATION:

FILING DATE: October 30, 1992 attorney/AGENT INFORMATION: NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/099002 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906

TELETAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 237

TYPE: nucleic acid STRANDEDNESS: double

Sequence 237 BP; 83 A; 38 C; 52 G; 64 T; 0 other; TOPOLOGY: linear

; 0 Query Match 46.2%; Score 12; DB 9; Length 237; Best Local Similarity 58.3%; Pred. No. 3.58e+01; 0; Mismatches 10; Indels 14; Conservative Matches

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Gaps

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US-08-026-320A-3 STANDARD; DNA; UNC; 360 BP

01-JAN-1900

Sequence 3, Application US/08026320A. Sequence 3, Application US/08026320A Patent No. 5419904

GENERAL INFORMATION:
APPLICANT: Irie, Reiko F
TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
TITLE OF INVENTION: SECRETING ANTI-CANGLIOSIDE ANTIBODY

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles STATE: California COUNTRY: United States of America ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1

APPLICATION NUMBER: US/08/026, 320A CURRENT APPLICATION DATA:

FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION: NAME: Oldenkamp, David J REGISTRATION NUMBER: 29421

TELECOMMUNICATION INFORMATION REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 3: TELEPHONE: 3107885046 TELEFAX: 3102771297

SEQUENCE CHARACTERISTICS: LENGTH: 360 base pairs STRANDEDNESS: single TOPOLOGY: linear TYPE: nucleic acid

MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO DRIGINAL SOURCE:

ORCANISM: Homo sapiens INDIVIDUAL ISOLATE: Epstein Barr Virus transformed B INDIVIDUAL ISOLATE: cell

CELL TYPE: B-cell

May 14 11:31 FLP.mi

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GENERAL INFORMATION:

APPLICANT: SHIRATORI, Toshikazu

APPLICANT: INOUE, Chihiro

APPLICANT: KITAGAWA, Yoshichika

APPLICANT: KUSANO, Toononobu

TITLE OF INVENTION: DNA FRACHENT COBING FOR MERCURIC REDUCTASE OF

TITLE OF INVENTION: THIOBACILLIUS, AND RECOMBINANT PLASMID

NUMBER OF SEQUENCES: 5 Gaps ; 0 Score 12; DB 10; Length 1229; Pred. No. 3.58e+01; 0; Indels LOCATION: 61..1056 Sequence 1229 BP; 413 A; 229 C; 261 G; 326 T; 0 other; ADDRESSEE: Nixon & Vanderhye, P.C. STREET: 1100 No. 5348888th Glebe Road, 8th Floor SOFTWARE: PatentIn Release #1.0, Version #1.25 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 PCT
TELECOMMUNICATION INFORMATION:
TELEPRONE: 201 487-5800
TELEFRAX: 201 343-1684 Mismatches US-08-133-347-3 STANDARD; DNA; UNC; 1635 BP. PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400 APPLICATION NUMBER: US 08/180, 209 OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 3, Application US/08133347. Sequence 3, Application US/08133347 Patent No. 5348888 COMPUTER: IBM PC Compatible INFORMATION FOR SEQ ID NO: 54: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk 11-JAN-1994 FILING DATE: 11-MAR-1993 ATTORNEY/AGENT INFORMATION: LENGTH: 1229 base pairs CURRENT APPLICATION DATA: Query Match 46.2%; Best Local Similarity 100.0%; Matches 12; Conservative TYPE: nucleic acid STRANDEDNESS: single CORRESPONDENCE ADDRESS: MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: CITY: Arlington STATE: Virginia COUNTRY: U.S.A. TOPOLOGY: linear 349 AATAGGAACTTC 360 TELEX: 133521 12 aataggaacttc 1 NAME/KEY: CDS FILING DATE: 01-JAN-1900 XXXXXX RESULT a g

MOLECULE TYPE: CDNA TOPOLOGY: linear

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FEATURE:

COUNTRY: USA ZIP: 94080

01-JAN-1900

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Gaps

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APPLICANT: IBEX TECHNOLOGIES and APPLICANT: ZIMMERMANN, Joseph TITLE OF INVENTION: Nucleic Acid Sequences And Expression TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Deriv PCT-US95-07391A-1 STANDARD; DNA; UNC; 2339 BP Sequence 1, Application PC/TUS9507391A. Sequence 1, Application PC/TUS9507391A GENERAL INFORMATION: 01-JAN-1900 | RESULT 33 | PCT-US9 | PC

OPERATING SYSTEM: PC_DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: TITLE OF INVENTION: Flavobacterium heparinum ADDRESSEE: Hale and Dorr STREET: 1455 Pennsylvania Avenue, N.W. APPLICATION NUMBER: PCT/US95/07391A MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible 09-JUNE-1995 CITY: Washington, D.C. COMPUTER READABLE FORM: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: COUNTRY: U.S.A. FILING DATE: 09 CLASSIFICATION: ZIP: 20004

PRIOR APPLICATION DATA:

May 14 11:31

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Gaps ; 0 Query Match 46.2%; Score 12; DB 11; Length 2339; Best Local Similarity 58.3%; Pred. No. 3.58e+01; 0; Mismatches 10; Indels Sequence 222, Application US/08105483.
Sequence 222, Application US/08105483
Patent No. 5494807.
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN MOLECULE TYPE: DNA (genomic) Sequence 2339 BP; 667 A; 469 C; 571 G; 632 T; 0 other; COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 US-08-105-483-222 STANDARD; DNA; UNC; 2356 BP. REFERENCE/DOCKET NUMBER: 104385.116PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (202)942-8400 NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: Now York
STATE: NY NAME: Frommer, William S. REGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 454310-2400 APPLICATION NUMBER: US 07/847,951 FILING DATE: 06-MAR-1992 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US/08/105,483 APPLICATION NUMBER: 08/258,639 2168 CTTTTCCGTTGTTGGTAAAGGAAC 2191 NAME: BAKER, Hollie L. REGISTRATION NUMBER: 31,321 ELECOMMUNICATION INFORMATION: 8 ctattcNNNNNNNNgtataggaac 31 TELEFAX: (202) 942-8484 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: FILING DATE: 10 JUNE 1994 FILING DATE: 12-AUG-1993 CLASSIFICATION: 424 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk ATTORNEY/AGENT INFORMATION: LENGIH: 2339 base pairs CURRENT APPLICATION DATA: TYPE: nucleic acid STRANDEDNESS: double 14; Conservative TOPOLOGY: linear COUNTRY: USA ZIP: 10036 xxxxxx 01-JAN-1900 Matches 쇰 ð 888888888888888888888888888888888

ö Gaps ; 0 Query Match 46.2%; Score 12; DB 4; Length 2356; Best Local Similarity 58.3%; Pred. No. 3.58e+01; Matches 14; Conservative 0; Mismatches 10; Indels APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCIEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation TOPOLOGY: linear Sequence 2356 BP; 761 A; 397 C; 340 G; 858 T; 0 other; PCT-US91-07035-11 STANDARD; DNA; UNC; 2679 BP. STREET: 1400 Fifty-third Street CITY: Emeryville STATE: California ZIP: 94608
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91/07035 FILING DATE: 19910930
CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA: FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523, 394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143, 441
FILING DATE: 12-JAN-1988 Sequence 11, Application PC/TUS9107035 Sequence 11, Application PC/TUS9107035 GENERAL INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987 APPLICATION NUMBER: US 590, 213 TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO: 222: SEQUENCE CHARACTERISTICS: 220 GAAATTCTTATACGTATCGGCGAA 243 34 gaagttcctatacNNNNNNngaa 11 TELEPHONE: (212) 840-3333 TELEFAX: (212) 840-0712 LENGTH: 2356 base pairs TYPE: nucleic acid STRANDEDNESS: single PRIOR APPLICATION DATA: 01-JAN-1900 RESULT 35 XXXXXX g 888888888

May 14 11:31 FLP.mi 36

CC FILING DATE: 22-AUG-1986 CC FILING DATE: 22-AUG-1986 CC PRIOR APPLICATION NUMBER: US 446,121 CC FILING DATE: 15-AUG-1991 CC FILING DATE: 15-AUG-1991 CC FILING DATE: 12-DEC-1990 CC FILING DATE: 21-DEC-1990 CC FILING DATE: 22-DEC-1990 CC FILING DATE: 20-SEP-1990 CC FILING DATE: 22-DEC-1990 CC FILING DATE: 22-DEC-1999 CC FILING DATE: 23-DEC-1999 CC FILING DATE: 24-JUL-1990 CC FILING DATE: 2679 DASE pairs CT FILING DATE: 2679 DASE pairs CC STRANDEDNESS: single CC STRANDEDNESS: Singl
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ö Gaps ö Sequence 111, Application PC/TUS9508071.
Sequence 111, Application PC/TUS9508071
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS: Query Match 46.2%; Score 12; DB 9; Length 2757; Best Local Similarity 56.3%; Pred. No. 3.58e+01; Matches 18; Conservative 0; Mismatches 14; Indels MOLECULE TYPE: DNA (genomic) Sequence 2757 BP; 693 A; 713 C; 809 G; 542 T; 0 other; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION: SOFTWARE: PatentIn Release #1.0, Version #1.25 6300 Sears Tower, 233 S. Wacker Drive ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER .r 37 PCT-US95-08071-111 STANDARD; DNA; UNC; 3033 BP. 169 AGTICCTGTGCCTTAAGAACATTAGAACCTTC 200 32 agttcctatacNNNNNNNNgaataggaacttc 1 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS REFERENCE/DOCKET NUMBER: 8586 400 Garden City Plaza TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 79: NTTORNEY/AGENT INFORMATION: NAME: DiGIGLIO, Frank S. REGISTRATION NUMBER: 31,346 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk SEQUENCE CHARACTERISTICS: LENGTH: 2757 base pairs TYPE: nucleic acid STRANDEDNESS: double Garden City CITY: Chicago STATE: Illinois COUNTRY: USA TOPOLOGY: linear COUNTRY: USA 90909 ZIP: 11530 STREET: 01-JAN-1900 XXXXXX RESULT g 9 88888888888888888888888888888888888888

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Query Match 46.2%; Score 12; DB 11; Length 3033; Best Local Similarity 57.7%; Pred. No. 3.58e+01; LOCATION: 138..2528 Sequence 3033 BP; 785 A; 723 C; 723 G; 802 T; 0 other; PRIOR DATE: 23 DEC 1993

PRIOR DATE: 32 DEC 1993

PRIOR DATE: 29 DEC 1992

ATTORNEY/ACENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32149

TELECOMMUNICATION INFORMATION:
TELEFRONE: 312/474-6300

TELEFAX: 312/474-0448

TELEFAX: 25-3856

INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993 APPLICATION NUMBER: PCT/US95/08071 LENGTH: 3033 base pairs CURRENT APPLICATION DATA: STRANDEDNESS: single TYPE: nucleic acid MOLECULE TYPE: cDNA FEATURE: TOPOLOGY: linear CLASSIFICATION: NAME/KEY: CDS FILING DATE: May 14 11:31

Gaps ö APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocadherin Materials and Methods 0; Mismatches 11; Indels ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & STREET: 6300 Sears Tower, 233 S. Wacker Drive JT 38 PCT-US95-08071-111 STANDARD; DNA; UNC; 3033 BP. Sequence 111, Application PC/TUS9508071. Sequence 111, Application PC/TUS9508071 GENERAL INFORMATION: 2787 TCATATTCGCTGTAACGAATTGGAAC 2812 6 tcctattcNNNNNNNNgtataggaac 31 NUMBER OF SEQUENCES: 115 CORRESPONDENCE ADDRESS: 15; Conservative CITY: Chicago STATE: Illinois COUNTRY: USA ADDRESSEE: Borun 01-JAN-1900 XXXXXX Matches 쇰 ð

SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

ZIP: 60606

APPLICATION NUMBER: PCT/US95/08071

May 14 11:31

APPLICANT: Thompson, Mark APPLICANT: Gaertner, Frank H. TITLE OF INVENTION: No. 5468483el Bacillus thuringiensis Isolate TITLE OF INVENTION: Having Anti-Protozoan Activity Gaps ö Query Match 46.2%; Score 12; DB 8; Length 3513; Best Local Similarity 59.1%; Pred. No. 3.58e+01; Matches 13; Conservative 0; Mismatches 9; Indels LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK CLONE: 81F Sequence 3513 BP; 1169 A; 592 C; 769 G; 983 T; 0 other; ADDRESSEE: Roman Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 US-08-278-685-1 STANDARD; DNA; UNC; 3513 BP ORGANISM: BACILLUS THURINGIENSIS COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: 97/828,788 Sequence 1, Application US/08278685. Sequence 1, Application US/08278685 Patent No. 5468483 GENERAL INFORMATION: TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3513 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double REFERENCE/DOCKET NUMBER: MA75 NAME: SALIWANCHIK, DAVID R. REGISTRATION NUMBER: 31,794 1744 GAACTICCTATICGIGGIG 1765 MOLECULE TYPE: DNA (genomic) INDIVIDUAL ISOLATE: PS81F IMMEDIATE SOURCE: 1 gaagttcctattcNNNNNNNg 22 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk ATTORNEY/AGENT INFORMATION: NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: CITY: Gainesville STATE: FL TOPOLOGY: linear HYPOTHETICAL: NO ANTI-SENSE: NO STRAIN: KENYAE COUNTRY: USA ORIGINAL SOURCE: FILING DATE: 2IP: 32606 01-JAN-1900 RESULT 40 XXXXXX 쉱 ò

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

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Score 12; DB 4; Length 3513; Pred. No. 3.58e+01; 9; Indels MOLECULE TYPE: DNA (genomic) Sequence 3513 BP; 1169 A; 592 C; 769 G; 983 T; 0 other; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: Two First National Plaza, 20 South Clark MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUFTWARY APPLICATION NATA:
FILING DATE: 19920420 APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
UDMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS: PCT-US92-03222-38 STANDARD; DNA; UNC; 4131 BP. Mismatches REGISTRATION NUMBER: 21,023
REFERENCE/DOCKET NUMBER: 07/654,166
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800 APPLICATION NUMBER: US 07/654,166 APPLICATION NUMBER: US/08/278, 685 FILING DATE: 12-FEB-1991 APPLICATION NUMBER: US 08/091,527 Sequence 38, Application PC/TUS9203222 Sequence 38, Application PC/TUS9203222 1744 GAACTICCIAIICGIGGIG 1765 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: APPLICANT: Beavo, Joseph A. FILING DATE: 12-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, Roman Bentley, Kelley LENGTH: 3513 base pairs Query Match 46.2%; Best Local Similarity 59.1%; TYPE: nucleic acid STRANDEDNESS: double PRIOR APPLICATION DATA: COMPUTER READABLE FORM: 13; Conservative CLASSIFICATION: 435 CITY: Chicago STATE: Illinois COUNTRY: USA TOPOLOGY: linear GENERAL INFORMATION: Street

ZIP: 60603

STREET:

APPLICANT: APPLICANT:

01-JAN-1900

RESULT 41 XXXXXX

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Query Match

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Matches

REFERENCE/DOCKET NUMBER: NU-9207 TELECOMMUNICATION INFORMATION: TELEPHONE: (312)-456-8000 TELEFAX: (312)-456-7776 TOPOLOGY: linear ZIP: 60606-4002 COUNTRY: USA 01-JAN-1900 XXXXXX Matches RESULT g ç, ö Gaps APPLICANT: Trustees of The University of Pennsylvania TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: and Pathogens NUMBER OF SEQUENCES: 82 CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris ; Query Match 46.2%; Score 12; DB 3; Length 4131; Best Local Similarity 60.0%; Pred. No. 3.58e+01; 0; Mismatches 8; Indels Sequence 4131 BP; 866 A; 1233 C; 1174 G; 858 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: .r 43 PCT-US95-07744A-15 STANDARD; DNA; UNC; 4146 BP. CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 53895/2nd, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822 STREET: One Liberty Place, 46th floor APPLICATION NUMBER: PCT/US95/07744A Sequence 15, Application PC/TUS9507744A. Sequence 15, Application PC/TUS9507744A GENERAL INFORMATION: COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: 08/261,822 FILING DATE: June 17, 1994 TELECOMMUNICATION INFORMATION: TELEX: . 25-3856
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs TELEPHONE: (312) 346-5750 TELEFAX: (312) 984-9740 FILING DATE: 15-JUNE-1995 Db 1742 TCCTATACAAGAAAGTGAAT 1761 29 tcctatacNNNNNNNNgaat 10 PRIOR APPLICATION DATA: TYPE: NUCLEIC ACID STRANDEDNESS: single NAME/KEY: CDS LOCATION: 148..2910 12; Conservative CITY: Philadelphia MOLECULE TYPE: CDNA TOPOLOGY: linear CLASSIFICATION: STATE: PA 01-JAN-1900 FEATURE XXXXXX Matches

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ö Gaps ; Query Match 46.2%; Score 12; DB 11; Length 4146; Best Local Similarity 58.3%; Pred. No. 3.58e+01; 0; Mismatches 10; Indels Sequence 4146 BP; 1265 A; 707 C; 744 G; 1430 T; 0 other; US-08-045-806-3 STANDARD; DNA; UNC; 5261 BP. 1610 TATACAAAAATAAAATGGGAACT 1633 REGISTRATION NUMBER: 34,293 TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4146 base pairs MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO TELECOMMUNICATION INFORMATION 26 tatacNNNNNNNNNgaataggaact 3 TELEPHONE: (215) 568-3100 ATTORNEY/AGENT INFORMATION: NAME: Beardell, Lori Y. TYPE: nucleic acid STRANDEDNESS: single 14; Conservative May 14 11:31 888888888888888888888888888888888

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APPLICANT: Poland, Alan TITLE OF INVENTION: Ah Receptor CDNA and Method of TITLE OF INVENTION: Determining Human Risks To Environmental Pollutant OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CORRESPONDENCE ADDRESS: ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut STREET: 100 South Macker Drive, Suite 960 Sequence 3, Application US/08045806.
Sequence 3, Application US/08045806
Patent No. 5378822
GENERAL INFORMATION:
APPLICANT: Bradfield, Christopher Alan
APPLICANT: Dolwick, Kristin Marie CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,806
FILING DATE: 19930408 31,327 COMPUTER: IBM PC compatible COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk ATTORNEY/AGENT INFORMATION: NAME: Fentress, Susan B. 23 REGISTRATION NUMBER: CLASSIFICATION: 435 NUMBER OF SEQUENCES: STREET: 100 South CITY: Chicago STATE: Illinois

FLP mi May 14 11:31

Sequence 8298 BP; 2180 A; 2086 C; 2039 G; 1993 T; 0 other; LOCATION: 731..5272

Gaps ö Query Match 46.2%; Score 12; DB 9; Length 8298; Best Local Similarity 59.1%; Pred. No. 3.58e+01; Matches 13; Conservative 0; Mismatches 9; Indels

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1231 CAGGGGCATGAACAGGAACTTC 1252

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Search completed: Tue May 14 11:40:38 1996 Job time: 10 secs.

May 14 13:48

SUMMARIES

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch nn

Run on:

Tue May 14 13:49:31 1996; MasPar time 32.48 Seconds 741.130 Million cell updates/sec

Tabular output not generated.

>FLP (1-34) from frt.seq 26 Description:

1 gaagttcctattcNNNNNNNNgtataggaacttc 34 Perfect Score: N.A. Sequence:

cttcaaggataagNNNNNNNNcatatccttgaag

TABLE default Scoring table:

Gap 10

Dbase 0; Query 0 Nmatch STD

264399 seqs, 353985056 bases x 2 Searched:

Post-processing: Minimum Match 08

Listing first 45 summaries

Database:

embl-newil 1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PRII 10:PRIZ 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN 16:UNC 17:VRT 18:VIR

Database:

genbank91
19;BCTI 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7
26:INVI 27:INV2 28:INV3 29:INV4 30:INV5 31:MAMI 32:MAM2
33:PAT1 34:PAT2 35:PAT3 36:PHG 37:PLN1 38:PLN2 39:PLN3
40:PLN4 41:PLN5 42:PLN5 43:PLN5 44:PRL1 45:PRL2 46:PRL3
47:PRL4 48:PRL5 49:PRL6 50:PRL7 51:PRL8 52:PRL9 53:ROD1
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 69:RD01
61:STN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5
66:VRL6 69:VRT1 70:VRT2 71:VRT3

genbank-newll 72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN 79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA Database:

86:VRL 87:VRT u-emb144_91

Database:

14-NOV-1994

PAT

ALI CAMENTS

68 bp DNA Sequence 1 from patent WO 8703006. 108526

DEFINITION ACCESSION KEYWORDS SOURCE

RESULT

ORGANISM REFERENCE

1 (bases 1 to 68) Unclassified. Unknown. Unknown.

88:part1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 7.033; Variance 2.584; scale 2.722

Statistics:

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	m	26	100.0	125		APDNATSR3	plasmid	.89e-
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	6	56	100.0	1888		CVPMAKC76	vector	9
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ပ	14	56	100.0	6010		YSCTRAM1	Cloning vector pYSVE2	4.89e-08
υ	12	56	100.0	6037	43	YSCTRAM2		4.89e-08
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c	6	26	100.0	6318		YSCPLASM		896
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	31	56	100.0			A19996		•
	35	56	100.0	7984		A18079	0	4.89e - 08
	33	56	100.0	8117		CVU29899	vector	4.89e - 08
U	34	56	100.0	8393	12	CV30497	vector	4.89e - 08
ပ	32	56	100.0	8393		CVU30497	Cloning vector pAS2-1	4.89e-08
ပ	36	56	100.0	10667		YEP213	pisomal	4.89e-08
υ	31	56	100.0	10667		YEP13	Yeast episomal vector	4.89e-08
U	38	22		200	-	YSCPL2M	Yeast (S.cerevisiae)	1.34e-04
	39	22	84.6	5616	61	PRS424	Yeast episomal vector	1.34e-04
	40	22	84.6	5726		PRS426	Yeast episomal vector	1.34e-04
v	41	22		6624	œ	CVU37458		1.34e-04
υ	42	22	•	6624		CV37458	Yeast CUP1 expression	P
	43	22	•	7834	-	337	t episomal	å
ပ	44	22	84.6	7859	88	999		ď
U	45		84.6	7984	34	A18079	yeast expression vect	1.34e - 04

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Snaith, M.R., Kilby, N.J. and Murray, A.H. An E. coli system for assay of FLP site-specific recombination on Snaith, M.R., Kilby, N.J. and Murray, A.H.
An E. coli system for assay of FLP site-specific recombination on substrate plasmids
Unpublished ö Snaith, University of Cambridge, Dept of Genetics, Downing Site, Downing Street, Cambridge CB2 3Eh, UK NCBI gi: 870843 Submitted (16-JUN-1995) to the EMBL/GenBank/DDBJ databases. M. Submitted (16-JUN-1995) to the EMBL/GenBank/DDBJ databases. M. 21-JUN-1995 21-JUN-1995 Gaps containing target site for specific APDNATSR1 154 bp DNA SYN 21-JUN-19 Artificial plasmid DNA containing target site for specific /note="5' modified portion fo beta-galactosidase" ; 0 /note="FRT target site" /bound_moiety="FLP site-specific recombinase" Score 26; DB 61; Length 125; Pred. No. 4.89e-08; 8; Indels /translation="MEKLLFRSSYSLESIGTSSLALA" beta-galactosidase; recombinase target site /organism="Artificial sequences" /note="pid:e; NCBI gi: 870844"
/codon_start=1 /product="beta-galactosidase" 0; Mismatches 75 gaagttcctattctctagaaagtataggaacttc 108 32 /evidence=experimental Location/Qualifiers 33 g Artificial plasmid DNA 125 bp recombinase (125 bp) Query Match 100.0%; Best Local Similarity 76.5%; recombinase (154 bp) 27 c (bases 1 to 154) (bases 1 to 125) (bases 1 to 125) (bases 1 to 154) 26; Conservative substrate plasmids Direct Submission 56..>125 Direct Submission 61..108 1..125unclassified. unidentified unidentified. unclassified. unidentified unidentified Unpublished APDNATSR3 Snaith, M. Snaith, M. 39 X87980 misc_feature misc binding source DEFINITION ORGANISM DEFINITION ORGANISM BASE COUNT TITLE JOURNAL Matches TITLE JOURNAL ACCESSION REFERENCE AUTHORS AUTHORS ACCESSION AUTHORS JOURNAL REFERENCE REFERENCE JOURNAL AUTHORS REFERENCE CDS KEYWORDS FEATURES KEYWORDS TITLE COMMENT TITLE RESULT SOURCE ORIGIN SOURCE LOCUS g ó

Fagrelius, T.J. and Livingston, D.M. Location of DNNase I sensitive cleavage sites in the yeast 2 mu-m plasmid DNA, chromosome ö [1] examines whether cleavage sites are specific when the DNA-associated protein is stripped away and draws the conclusion that the specificity of DNAase I is dependent on the presence of Snaith, University of Cambridge, Dept of Genetics, Downing Site, Downing Street, Cambridge CB2 3Eh, UK NCBI gi: 870840 YSCPL2M 200 bp DNA PLN 10-DEC-1984 Yeast (S.cerevisiae) 2 micron plasmid (A-form) inverted repeat Gaps Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Endomycetales; /note="5' modified portion fo beta-galactosidase" 61..108 ö /bound_moiety="FLP site-specific recombinase" feast (Saccharomyces cerevisiae) 2 micron plasmid DNA Score 26; DB 61; Length 154; Pred. No. 4.89e-08; Length 200 Indels /organism="Saccharomyces cerevisiae" /translation="MÉKLLFRSSYSLESIGTSERF" 56..154 ä /organism="Artificial sequences" Score 26; DB 43; Pred. No. 4.89e-08; /note="pid:e; NCBI gi: 870841' /product="beta-galactosidase" 0; Mismatches 39 t 50 t 75 gaagttcctattctctagaaagtataggaacttc 108 1 gaagttcctattcNNNNNNNNgtataggaacttc 34 /note="FRT target site" = = = = = /evidence=experimental J. Mol. Biol. 173, 1-13 (1984) 84138647 57 a 47 c 46 g 103 bp upstream of Xbal site. /note="plasmid DNA" 56..>118 Location/Qualifiers Location/Qualifiers 37 g Saccharomyces cerevisiae /codon_start=1 Query Match 100.0%; Best Local Similarity 76.5%; Query Match 100.0%; Best Local Similarity 76.5%; 37 c 26; Conservative Saccharomycetaceae. (bases 1 to 200) 1..2001..154 NCBI gi: 172188 nucleoprotein. = = = = = æ 41 region. plasmid. K01710 misc feature misc_binding 2 source BASE COUNT ORIGIN source DEFINITION ORGANISM Matches BASE COUNT ACCESSION REFERENCE AUTHORS JOURNAL MEDLINE CDS FEATURES FEATURES KEYWORDS TITLE COMMENT ORIGIN RESULT SOURCE 용 ð

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1 gaagttcctattcNNNNNNNNgtataggaacttc 34

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RESULT

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Sequencing long DNA fragments cloned in bacteriophage M13 by using internal primers. The sequence analysis of a yeast DNA fragment ö SCPLA1 1019 bp DNA PLA 06-JUL-1989 Part of the 2 micron plasmid of yeast encompassing one of the Sequence of 1019 nucleotides encompassing one of the inverted Gaps 13-JUL-1983 Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Eumycota; Ascomycotina; Hemiascomycetes; Saccharomycetales; Eumycota; Ascomycotina; Hemiascomycetes; Saccharomycetales; ö Query Match 100.0%; Score 26; DB 41; Length 1019; Best Local Similarity 76.5%; Pred. No. 4.89e-08; 1 others 8; Indels SCOR01 1578 bp DNA PLAN Yeast sequence containing a replication origin. V01317 /organism="Saccharomyces cerevisiae" /organism="Saccharomyces cerevisiae" repeats from the yeast 2 micrometer plasmid Nucleic Acids Res. 7 (2), 361-375 (1979) ىد 0; Mismatches 299 gaagtteetataetttetagagaataggaaette 332 /plasmid="2 micron plasmid" 192 c 225 g 330 t Biochem. J. 199 (3), 819-823 (1981) Saccharomycetaceae; Saccharomyces. Saccharomycetaceae; Saccharomyces. containing a replication origin Location/Qualifiers 306 g Location/Qualifiers KST SCE.PLASMID (INCOMPL.). Hindley, J. and Phear, G.A. Saccharomyces cerevisiae Hindley, J. and Phear, G.A. Saccharomyces cerevisiae origin of replication. (bases 1 to 1578) (bases 1 to 1019) 26; Conservative 301 c inverted repeats. 1..1578 terminal repeat. 1..1019baker's yeast. baker's yeast. NCBI gi: 4083 NCBI gi: 4181 æ æ 80034481 82182087 445 271 V01322 DEFINITION source sonrce ORGANISM DEFINITION ORGANISM BASE COUNT BASE COUNT JOURNAL MEDLINE ACCESSION REFERENCE AUTHORS JOURNAL MEDLINE ACCESSION REFERENCE AUTHORS KEYWORDS KEYWORDS FEATURES FEATURES TITLE TITLE COMMENT COMMENT SOURCE ORIGIN SOURCE ORIGIN LOCUS g გ

100.0%; Score 26; DB 41; Length 1578;

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gaagttcctattctctagaaagtataggaacttc 123

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Pred. No. 4.89e-08;

Best Local Similarity 76.5%;

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LSSHLADAGKVSIMADAMRRIJTIDPATCPFDHQAKHRIERARTRMEAGIVDQDDI.DE EHQGIAPAELFARIKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDGGRIGVADRY QDIALATRDIAEELGGEMADRFLVIXGIAAPDSQRIAFYRLI.DEFF" /translation="Miexdelhacspaawverlegymaqot1ccsdaavfrlsaqcr pvlevktdlsgalmelloebaarlsmlattgvpcaavldvvteagrdmlllgevpcqdl ö 'note="SP6 RNA polymerase transcription initiation site' /note="T7 RNA polymerase transcription initiation site" Submitted (07-APR-1994) Gyorgy Posfai, University of Misconsin, McArdle Laboratory for Cancer Research, 1400 University Avenue, Madison, MI 53706, USA CVPMAKK76 1814 bp DNA circular SYN 16-SEP-1994 Cloning vector pWAKK76 with kanamycin phosphotransferase (KnR) Artificial sequence; Cloning vector. 1 (bases 1 to 1814) Posfai, G., Koob, M., Hradecna, Z., Hasan, N., Filutowicz, M. and Gaps In vivo excision and amplification of large segments of the ö 'note="FRT site from yeast 2 micron plasmid" /note="gamma replication origin from R6K" Indels 'product="kanamycin phosphotransferase" standard name="multiple cloning site" Nucleic Acids Res. 22 (12), 2392-2398 (1994) /organism="Cloning vector pMAKK76" /lab_host="Escherichia coli" /codon_start=1 /function="kanamycin resistance" Pred. No. 4.89e-08; 1199 gaagtteetataetttetagagaataggaaette 1232 0; Mismatches /note="NCBI gi: 475709" /evidence=experimental complement (869..1663) /gene="KnR" Location/Qualifiers /transl table=11 complement (174) /direction=LEF1 gene, complete sequence. Cloning vector pMAKK76. Cloning vector pMAKK76 /plasmid="" (bases 1 to 1814) Best Local Similarity 76.5%; 459 c Conservative Direct Submission 112..168430..805 Escherichia coli 1..1814NCBI gi: 475708 Szybalski, W. Posfai, G. 94310070 463 008460 26; misc_feature misc feature misc_feature misc feature rep origin source DEFINITION ORGANISM BASE COUNT Matches JOURNAL ACCESSION AUTHORS REFERENCE AUTHORS JOURNAL MEDLINE REFERENCE CDS KEYWORDS FEATURES TITLE COMMENT SOURCE ORIGIN

/translation="MEXKITCYTTVDISQMHRKEHFEAFQSVAQCTYNQTVQLDITAF
LKTVKKNKHKFYPAFIHILARLANAHPKFRAAMKDGELVIMDSVHPCYTVFHEQTETF
SSLMSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPMVSFTSFDLNV
ANMDNFFAPVFTMCKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEMQGG CVPMAKC76 1888 bp DNA circular SYN 16-SEP-1994 Cloning vector pWAKC76 with chloramphenicol acetyltransferase (CmR) /note="SP6 RNA polymerase transcription initiation site" 430..805 ö /note="T7 RNA polymerase transcription initiation site" Submitted (07-APR-1994) Gyorgy Posfai, University of Wisconsin, McArdle Laboratory for Cancer Research, 1400 University Avenue, Gaps Posfai, G., Koob, M., Hradecna, Z., Hasan, N., Filutowicz, M. and In vivo excision and amplification of large segments of the ö /product="chloramphenicol acetyltransferase" /note="FRT site from yeast 2 micron plasmid" /note="gamma replication origin from R6K" Indels /standard name="multiple cloning site" /function="chloramphenicol resistance" Nucleic Acids Res. 22 (12), 2392-2398 (1994) /organism="Cloning vector pMAKC76" /lab host="Escherichia coli" Mismatches Artificial sequence, Cloning vector. 1 gaagttcctattcNNNNNNNNNNgtataggaacttc 34 17 gaagttcctattctctagaaagtataggaacttc 50 553 /note="NCBI gi: 475711" /evidence=experimental complement (930..1589) Location/Qualifiers б 409 /transl table=li /direction=LEFT gene, complete sequence. Escherichia coli qenome Cloning vector pMAKC76. Madison, WI 53706, USA NCBI gi: 475710 /codon start= /plasmid="" /gene="CmR" (bases 1 to 1888) (bases 1 to 1814) 399 c Conservative 112..168 Direct Submission 1..1888 Szybalski, W. Posfai, G. 94310070 527 008461 misc_feature misc_feature misc_feature misc_feature rep origin 6 source DEFINITION ORGANISM BASE COUNT TITLE JOURNAL Matches REFERENCE AUTHORS ACCESSION AUTHORS JOURNAL REFERENCE FEATURES 9 KEYWORDS TITLE COMMENT g ð

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ö Gaps ö Score 26; DB 61; Length 5616; Pred. No. 4.89e-08; 0; Mismatches 8; Indels Query Match 100.0%; Best Local Similarity 76.5%; 26; Conservative Matches

5169 gaagttcctatactttctagagaataggaacttc 5202

34 gaagttcctatacNNNNNNNNgaataggaacttc 1 g, PRS426 5726 bp DNA circular SYN 24-MAY-1995 Yeast episomal vector pRS426 with URA3 marker, complete sequence. UO3451 A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989) 89276910 artificial sequence; cloning vectors. 1 (bases 1 to 5726) Sikorski, R.S. and Hieter, P. Cloning vector pRS426. Cloning vector pRS426 DEFINITION ACCESSION RESULT 11 ORGANISM AUTHORS JOURNAL MEDLINE REFERENCE KEYWORDS TITLE SOURCE

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Gaps

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8; Indels

0; Mismatches

26; Conservative

Matches

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2 (bases 1 to 5726)

REFERENCE

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Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake City, UT 84132 USA and Molecular Biology, University of Utah Medical Center, Salt Lake Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral ö PRS423 5797 bp DNA circular SYN 24-MAY-1995 Yeast episomal vector pRS423 with HIS3 marker, complete sequence. U03454 A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989) Gaps Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and ö Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. Multifunctional yeast high-copy-number shuttle vectors Gene 110 (1), 119-122 (1992) Multifunctional yeast high-copy-number shuttle vectors 100.0%; Score 26; DB 61; Length 5797; 76.5%; Pred. No. 4.89e-08; Score 26; DB 61; Length 5726; Pred. No. 4.89e-08; 8; Indels /organism="cloning vector pRS423" 1536 a 1308 c 1374 g 1579 t /organism="cloning vector pRS426" 1246 c 1370 g 1542 t 0; Mismatches 5279 gaagttcctatactttctagagaataggaacttc 5312 artificial sequence; cloning vectors. 34 gaagttcctatacNNNNNNNNNgaataggaacttc 1 Location/Qualifiers Location/Qualifiers Gene 110 (1), 119-122 (1992) Sikorski, R.S. and Hieter, P. Cloning vector pRS423. Cloning vector pRS423 Query Match 100.0%; Best Local Similarity 76.5%; (bases 1 to 5797) 3 (bases 1 to 5797) 3 (bases 1 to 5726) (bases 1 to 5797) Best Local Similarity 76.5%; 26; Conservative City, UT 84132 USA Direct Submission Direct Submission 1..5797 1..5726 NCBI gi: 416325 NCBI gi: 416322 Stillman, D.J. Stillman, D.J. 1568 a Hieter, P. Hieter, P. 89276910 92184105 92184105 **Ouery Match** sonrce RESULT 12 source DEFINITION BASE COUNT Matches ORGANISM BASE COUNT TITLE JOURNAL TITLE MEDLINE AUTHORS JOURNAL ACCESSION REFERENCE AUTHORS AUTHORS JOURNAL AUTHORS REFERENCE JOURNAL MEDLINE REFERENCE MEDLINE REFERENCE AUTHORS FEATURES KEYWORDS FEATURES TITLE TITLE TITLE COMMENT COMMENT ORIGIN SOURCE 셤 g

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3139 gaagttcctatactttctagagaataggaacttc 3172 DEFINITION BASE COUNT ORGANISM REFERENCE AUTHORS JOURNAL ACCESS 10N JOURNAL MEDLINE REFERENCE AUTHORS KEYWORDS FEATURES CDS CDS TITLE TITLE COMMENT ORIGIN RESULT SOURCE д අ გ g The pF145L was constructed from pUC19 plasmid where two alu I sites were modified. The site 629 was replaced by a BqlII linker and the site 147 by a Clai site. The yeast selectable marker has been cloned in the BqlII site and the 2 micron 2.2 kb EcoRI fragment containing ORI and STB gene has been cloned at the Clai site. The pF145L is described in Bonneaud et al (1991): A family of low and high copy replicative, integrative and single-stranded High-frequency transformation of yeast: autonomous replication of Submitted (01-JUN-1993) to the EMBL/GenBank/DDBJ databases. Ozier-Kalogeropoullos O., CGM, CNRS, 91190 Gif sur Yvette, France artificial sequence; cloning vectors.

1 (bases 1 to 644; 1484 to 1610; 3862 to 5807)

Yanisch-Perron,C., Vieira,J. and Messing,J.

Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors

Gene 33 (1), 103-119 (1985) 15-AUG-1995 Bonneaud, N., Ozier-Kalogeropoulos, O., Li, G.Y., Labouesse, M., A family of low and high copy replicative, integrative and multicopy Saccharomyces cerevisiae/E. coli shuttle vector. Chevalier, M.R. and Lacroute, F. Trancriptional and traductional expression of a chimeric S.cerevisiae/E.coli shuttle vectors. YEAST, 7, 609-615. Proc. Natl. Acad. Sci. U.S.A. 76 (3), 1035-1039 (1979) single-stranded S. cerevisiae/E. coli shuttle vectors Struhl, K., Stinchcomb, D.T., Scherer, S. and Davis, R.W. Score 26; DB 61; Length 5807; Pred. No. 4.89e-08; 2-micron yeast replication origin; pUC19 plasmid; e-mail:odile%FRCGM51.BITNET@vm.gmd.de Minvielle-Sebastia, L. and Lacroute, F. 5351 gaagttcctatactttctagagaataggaacttc 5384 1344 g 1647 t 34 gaagttcctatacNNNNNNNNNgaataggaacttc 1 /organism=*Cloning vector bacterial- yeast plasmid in yeast Gene 1, 11-19 (1980) Location/Qualifiers DNA Yeast 7 (6), 609-615 (1991) Ozier-Kalogeropoullos, O. TRP1 selectable marker. (bases 1610 to 3862) 2 (bases 644 to 1484) 5807 bp hybrid DNA molecules (bases 1 to 5807) Query Match 100.0%; Best Local Similarity 76.5%; (bases 1 to 5807) 1261 c Direct Submission 1..5807 cloning vectors. cloning vectors NCBI qi: 397132 æ CVPFL45L 85180545 19180126 92116645 1555 X70267 source 13 DEFINITION BASE COUNT ORGANISM REFERENCE AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL JOURNAL REFERENCE MEDLINE JOURNAL AUTHORS JOURNAL REFERENCE MEDLINE AUTHORS AUTHORS ACCESSION REFERENCE MEDLINE REFERENCE FEATURES KEYWORDS TITLE TITLE TITLE SOURCE ORIGIN

YSPVTEKHLTDGMTVRELCSAA ITMSDNTAANLLLTTI CGPKELTAFLHNMGDHVTRL DRMEPELMEA IPNDERDTTMPVAMATTILKKLLTGELLTLASRQQ LIDMMEADKVAGPL LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA IELDIANSCKI LESFRPEERFPMMSTFKVLLCGAVLSR IDAGQEQLGRRIHYSQNDLVE /translation="msvinfTgssGPLVKVCGLQsTEAAECALDsDADLLGIICVPNR KRTIDPVIARKISSLVKAYKNSSGTPKYLVGVFRNQPKEDVLALVNDYGIDIVQLHGD ESMQEYQEF IGLEV IKRIUFPKDGNI LISAASQKPHSF IP LFDS EAGGTGELLDMNS I SDWYGRQESPES LHFMLAGGI FPENYGDALRIAGVI GYDVSGGYETNGVKDSNK IANF /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY Submitted (26-JUL-1991) Martin L. Pall, Department of Genetics and Cell Biology, Washington State University, Pullman, WA 99164-4234, A series of yeast vectors for expression of cDNAs and other DNA Gaps YSCTRAM1 6010 bp DNA PLN 18-JUI Cloning vector pYSVE2 TRP1 and AMPr genes, complete cds. ö Query Match 100.0%; Score 26; DB 43; Length 6010; Best Local Similarity 76.5%; Pred. No. 4.89e-08; Matches 26; Conservative 0; Mismatches 8; Indels Undels 1 /note="putative; NCBI gi: 173016" NCBI gi: 173017" construct; Artificial sequences 5039 gaagttcctatactttctagagaataggaacttc 5072 1385 g 1696 t 34 gaagttcctatacNNNNNNNNNNgaataggaacttc 1 34 gaagttcctatacNNNNNNNNNgaataggaacttc 1 /note="cloning vector" complement (1868..2728) Location/Qualifiers /organism="pYSVE2" Brunelli, J.P. and Pall, M.L. /note="putative; Yeast 9, 1299-1308 (1993) 94205259 /trans1 table=11 /trans] table=11 /codon_start=1 /gene="TRP1" /gene="AMPr" AmpR gene; TRP1 gene. pYSVE2. 1629 a 1300 c EIGASLIKHW" (bases 1 to 6010) (bases 1 to 6010) Synthetic construct 3041..3715 Direct Submission 1..6010 NCBI gi: 173015 Synthetic sednences Pall, M. L. M74015 14 source

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Matches

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RESULT 15 LOCUS DEFINITION ACCESSION	YSCTRAM2 6037 bp DNA PIA 18-JUL-1994 Cloning vector pYADE4 TRP1 and AMPr genes, complete cds. M74016	SOURCE ORGANISM	ukas selec cloning ve cloning ve artificial
KEYWORDS SOURCE ORGANISM	Arrystone; TRP1 gene. pYADE4. Synthetic construct	REFERENCE AUTHORS TITLE	1 (bases Yanisch-Pe Improved M
REFERENCE AUTHORS TITLE	Synthetic construct; Artificial sequences. 1 (bases 1 to 6037) Brunelli,J.P. and Pall,M.L. A series of yeast shuttle vectors for expression of cDNAs and other	JOURNAL MEDLINE REFERENCE ATTENDE	sequences Gene 33 (1 85180545 2 (bases
JOURNAL MEDLINE	Not Sequences Yeast 9 (12), 1299-1308 (1993) 94205259 7 (Apages 1 to 6037)	TITLE	Evidence f decarboxyl
AUTHORS TITLE JOURNAL	<pre>L \dassa 1 to 003/, Pall.M.L. Direct Submission Submitted (26-JUL-1991) Martin L. Pall, Department of Genetics and Cell Biology, Washington State University, Pullman, WA 99164-4234, nea</pre>	JOURNAL MEDLINE REFERENCE AUTHORS TITLE	Proc. Natl 79137106 3 (bases Chevalier, Trancripti
COMMENT	NCBI gi:	JOURNAL	bacterial- Gene 1, 11
source		HELERANCE AUTHORS TITLE JOURNAL	4 (bases Ozier-Kalo Direct Sub Submitted
	/gene=_AMrr_ /note="putative; NCBI gi: 387897" /codon_start=1 /transf_table=1	REFERENCE AUTHORS	ozier-halo e-mail:odi 5 (bases Bonneaud, N
S	A TAING BATLON-"BLIGHT WALLIFF FAR CLEV FAHE FILM WAY DALDGUARWGI IELDLANG GY LESFRPERFERPMSTFKYLLCGAY FIRD AGGOGGGGRIHYS OND LVE YSPYTEKHLTDGATVRELCSAR THYSONTAAULLITIG GEKELTAR LINNGOHYTR. DRWEPELHEA I PUDERD TWEPVAMATTLRKLLTGELLT LASRQQLIDWHEADKYAGP L IRSALBAGNFIADKSGAGERGSRGIIAALGPDGKPSRIUVIYTTGSQATWDERNRQIA 3041 3142	TITLE JOURNAL MEDLINE COMMENT	Minvielle- A family o single-str Yeast 7 (6 92116645 The pFL44L
3	/gene="TRP1" /hote="putative. start; NCBI gi: 912422" /codon start=1 /transl_except=(pos:30413043,aa:0THER) /transl_table=11 /translation="MKHTRAAMSMSVINFTGSSGPLWKVCGLQSTEAAECALDSDADL /translation="MKHTRAAMSMSVINFTGSSGPLWKVCGLQSTEAAECALDSDADL IGITCWPRRKTIDPVTARKISSLWKAYRNSSGTPKKILVGVFRNQPKEDVLALWNDYG IDIVQLHGDESWQEYGELGLEVIKRLVFPKDCNILLSAASQKPHSFIPLFDSEAGGT GELLDANSISDAVGRQESPESLHFMLAGGLTPENVGDALRIANGVIGVDVSGGVETNGV	FEATURES	
BASE COUNT ORIGIN	MDSNKAMPEVKNAMF. 1667 a 1270 c 1359 g 1741 t	BASE COUNT	1607 a
Query Mato Best Local Matches	Query Match 100.0%; Score 26; DB 43; Length 6037; Best Local Similarity 76.5%; Pred. No. 4.89e-08; Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	Query Match Best Local	Ouery Match Best Local Similarit Matches 26: Cons
Db 5066 ge I	5066 gaaqttectatactitetagagaataggaactie 5099 	Db 3395 g	3395 gaagttcctata
RESULT 16 LOCUS DEFINITION ACCESSION KEYMORDS	CVPFL44L 6063 bp DNA SYN 15-AUG-1995 multicopy Saccharomyces cerevisiae/E. coli shuttle vector. X70484 2-micron yeast replication origin; pUC19 plasmid;	RESULT 17 LOCUS DEFINITION ACCESSION	SCA21 2 micron p V01323 J01

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SOURCE	URA3 selectable marker. cloning vectors.
ORGANISM	cloning vectors
REFERENCE	archilotal sequence; cloning vectors. 1 (bases 1 to 641; 1743 to 1863; 4121 to 6063)
AUTHORS	
TITLE	<pre>improved Mis phage cloning vectors and host strains: nucleotide sequences of the Mismpl8 and pUC19 vectors</pre>
JOURNAL	Gene 33 (1), 103-119 (1985)
MEDLINE	85180545 2 (bases 644 to 1740)
AUTHORS	ach, M.L., Lacroute, F. and Botstein, D.
TITLE	orotidine-5
	by nybridizatio in Escherichia
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 76 (1), 386-390 (1979)
MEDLINE	/913/106 3 (bases 1866 to 4118)
AUTHORS	nevalier, M.R. and Lacroute, F.
TITLE	Trancriptional and traductional expression of a chimeric
TOTIBNAT.	Dacterial- yeast plasmid in yeast Cane 1: 11-19 (1980)
REFERENCE	4 (bases 1 to 6063)
AUTHORS	Ozier-Kalogeropoullos, O.
TITLE	Direct Submission Submitted (Al-HIN-1993) to the FMRI/GenBank/DDR.1 databases.
TUNIOO	Ozier-Kalogeropoullos O., CGM, CNRS, 91190 Gif sur Yvette, France
	.BITNET@vm.gmd.de
REFERENCE	
AUTHORS	Bonneaud, N., Uzier-Kalogeropoulos, U., Ll, G.I., Labouesse, M., Minvielle-Sebastia. L. and Lacroute. F.
TITLE	
INIMITAL	single-stranded S. cerevisiae/E. coli shuttle vectors
JOURNAL	Yeast (6), 6U9-613 (1991) 92116645
COMMENT	The pFL44L was constructed from pUC19 plasmid where two alu I sites
	site 141 by a Cial site. The yeast selectable marker has been
	cioned in the billi site and the 7 miclon 2:2 AD Econi Liaguent containing ORI and STB gene has been cloned at the Clai site. The
	pFL44L is described in Bonneaud et al (1991): A family of low and
	nign copy replicative, integrative and single-standed S.cerevisiae/E.coli shuttle vectors. YEAST, 7, 609-615.
	NCBI gi: 312626
FEATURES	Location/Qualifiers 16063
BASE COUNT ORIGIN	1607 a 1385 c 1307 g 1764 t
Query Match	100.0%;
Mest Local	Similarity 15.3%; Fred. No. 26; Conservative 0; Misma
0b 3395 g	tttctaga
Cp 34 g	
RESULT 17	
ACCESSION	V01323 J01347 L00321 L00322 L00323 L00324 M10185 M11111 M11593

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REFERENCE 11 (sites) AUTHORS McLeod, M., Craft, S. and Broach, J.R. TITLE Identification of the crossover site during FLP-mediated	recor circ]	JOURNAL MOI. Cell. Biol. 6, 3357-3367 (1986) MEDLINE 87089667 COMMENT (8) sites; mRNA CAP sites and poly-adenylation sites. [9] sites;	70 70	admic tream topy sequence for for homer by observed by become admic tream of 4-JMM-1986. Yeast 2 micron plasmid contains two 599 bp inverted repeats	separated by a large unique (UL) and a small unique (US) region. During recombination the UL and US regions invert producing two	sequence forms that differ in the orientation of one unique region relative to the other. The A form is presented below. FLP is the	only 2-micron circle-encoded protein needed for specific site recombination between the IRs of 2-micron circle. The minimal size of the recombination site remained for afficient FIP	recombinate catalysis of ecombination in vitro is no more than 28 bp, which includes note of two 12 hp invitro and constitution.	690-702 and 711-723 and all of an be spaced (703-710) [5].	Fig. recombinate cleaves the UNA at the boundaries of the spacer and becomes covalently linked to the space DNA [5], [9]. The	recombinant site is increased or decreased by 1 bp, while the spacer in the second site is unaltered [5]. Recombination between two sites with identical 1-base pair additions or deletions is relatively unaffected, suggesting that pairing of sequences in the spacer regions is important in FiP-promoted recombination events [5]. The sequence asymmetry utilized by the recombinase to determine the orientation of the site is located uniquely within	the spacer region. Another 13 bp direct repeat, is found at positions 676-688 [5]. FLP-mediated recombination involving two	Fur sites that are inverted with respect to each other results in inversion of the DNA sequences between the sites [4]. If the	participating recombination sites are in direct offendation, Fur promotes only the excision of the intervening DNA sequences [4]. The Rep 1 and Rep proteins are involved plasmid partitioning and	protein stability. A start codon in phase with the Repl coding region is located at A start codon in phase with the Repl coding region is located positions 1966-1964. Two CAP sites for Repl mRNA are located beyond the 'atg' codon (position 2008) at positions 2004 and 2005. Complete source information:	Yeast (S.cerevisiae, strain A364A D5) DNA, clones pJDB71 [1],	poz-os (z.), vezo (s.), parazz (s.), pozzo (s.), pozso (s.).	FEATURES Location/Qualifiers source 16318	/ Organism= 'Saccharomyces cerevisiae' exon	CONTLICT	i co		

/translation="mngerliaglimohfopmyydesrcviettrgffpypdnyk KYKTlafafyghulntddfpyjekeldmpdpalyyntivdriinhpelsofisvafis Olkatigegldinykgtlarrkkgirrpkgvffrymespfvntkytaffsylrdynki ASEYHNNTKFILIFSCQAYMASGPNFSALKNVIRCSIIHEYISKFVEREQDKGHIGDO ELPPEEDPSREIMNVQHEVNSLTEQDAEADEGLMGEIDSLCEKWQSEAEDQTEAEIIA DRIIGNSQRMANIKIRRTKFKSVLYHIIKELIQSQGTVKVYRGSSFSHDSIKISLHYE /translation="MPYKTAIDCIEELATQCFLSKLTDDDVSTFRRVCSKENDIIKLA LRIPRTIDYTSIIRLLYDT1PLASLSFNEALPLFCYSIDPAQQRQCDLRFYLRDVVKL ARPRKRLEMQKALLQWLPSLLSDVTLQIINDIRIRFEEIQPNIRQTVLQIYDRTCYPS /note="FLP recombinase binding site A [9]" /note="FLP-recombinase binding site B [9]" EQHITAVWYYLTVKFEEHWKPVDVEVEFRCKFKERKVDG" /note="Rep 1 protein; NCBI gi: 172192" 2254..2841 /note="D mRNA (alt.; 5' end +/- 3 bp)" /note="D mRNA (alt.; 5' end +/- 3 bp)" /note="D protein; NCBI gi: 172193" replace((622.624)..(622.624),"") /citation=[1] replace((665.666)..(665.666),"") /bound_moiety="FLP recombinase" replace((793.794)..(793.794),"") /note="REP2 mRNA (major alt.)"
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/note="REP2 mRNA (minor alt.)"
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/note="Repl mRNA (alt.)"
complement (836..2017)
/note="Repl mRNA (alt.)"
complement (836..2019) /note="Repl mRNA (alt.)" complement (887..2008) /note="Rep1 mRNA (alt.)" /note="Repl mRNA (alt.)" /note="Rep1 mRNA (alt.)" INFEHPNLGVFPETDSIFEPV* 3714..4312 /note="IR1" complement (4108..5184) complement (836..2010) complement (836..2004) complement (836..2005) replace(561, "") /citation=[1] /codon start=1 /codon start=1 /citation=[1] /citation=[1] /citation=[1] replace (642, 2254..2861 2271..2816 3930..3979 673..72 io pu. Ę.

Query Match

Best Local Similarity

Matches

26;

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Pred. No. 4.89e-08; Score 26; <u>,</u>,

DB 43;

Length 6318; Indels

Mismatches

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Nucleic Acids Res. 7, 361-375 (1979)
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Determination of DNA sequences essential for FLP-mediated
                     Gronostajski, R.M. and Sadowski, P.D.
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Yeast (S.cerevisiae, strain A364A D5) DNA, clones pJDB71 [1], p82-6B [2], CV20 [3], pMMD2 [4], p6P20 [5], pJFS166 [10].

Complete source information: positions 1966-1964. beyond the 'atg' code

codon

Two CAP sites for Repl mRNA are located (position 2008) at positions 2004 and

2005.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI gi: 172190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety="FLP recombinase" replace((793.794)..(793.794),"")
                                        /note="D protein; NCBI gi: 172193"
                                                                                                                                                                                  EQH I TAVWVY LTVKFEEHWKPVDVEVEFRCKFKERKVDG
                                                                                                                                                                                                         DRIIGNSQRMANLKIRRTKFKSVLYHILKELIQSQGTVKVYRGSSFSHDSIKISLHYE
                                                                                                                                                                                                                               ELP PEEDP SRELNNVQHEVNS LTEQDAEADEGLWGEIDS LCEKWQSEAEDQTEAE II A
                                                                                                                                                                                                                                                 ASEYHNNTKFILTFSCQAYWASGPNFSALKNVIRCSIIHEYISKFVEREQDKGHIGDQ
                                                                                                                                                                                                                                                                        QLKAT1GEGLDINVKGTLNRRGKGIRRPKGVFFRYMESPFVNTKVTAFFSYLRDYNKI
                                                                                                                                                                                                                                                                                          KYKTLAFAFVGHVINTDDTPVIEKELDWPDPALVYNTIVDRIINHPELSQFISVAFIS
                                                                                                                                                                                                                                                                                                                                                                             complement (887..2008)
                                                                                                                                                                                                                                                                                                                                                                                                                            complement (836..2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (836..2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (836..2010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (836..2019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (836..2017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (836..2038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="FLP recombinase binding site A [9]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace((665.666)..(665.666),"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace (642, "")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace((622.624)..(622.624), "")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace (561, "")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace (558, **)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace((464.466)..(464.466),"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="IR2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace((289.290)..(289.290), "")
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace((157.160)..(157.160), "")
/translation="MPYKTAIDCIEELATQCFLSKLTDDDVSTFRRVCSKENDIIKLA
                          /codon_start=
                                                                                       /note="D mRNA (alt.; 5'
                                                                                                                                                                                                                                                                                                              translation="MNGERLLACIKQCIMQHFQPMVYDESRCVIETTRGTFPVPDNYK/
                                                                                                                                                                                                                                                                                                                                   /codon_start=]
                                                                                                                                                                                                                                                                                                                                                         /note="Rep 1 protein;
                                                                                                                                                                                                                                                                                                                                                                                                      /note="Repl mRNA (alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Rep1 mRNA (alt.)"
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                                                                                                                                      'note="D mRNA (alt.; 5' end +/- 3 bp)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (alt.)*
                                                                                                                                                                                                                                                                                                                                                         NCBI gi: 172192"
                                                                                           end +/- 3 bp) "
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                                                                                                                                                                                                                                                                                                                                  COMMENT
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MEDLINE
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TITLE
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Best Local Similarity 76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 micron plasmid of yeast (circularly closed).

701323 J01347 L00321 L00322 L00323 L00324 M10185 M11111 M11593

M14239 M14240 M14241 M14242 M14243 M14244 M14245 M14253 M14254

M14255 M14256 M14257 M14258 M14259 M14591 M14592 M14593 M14594

M14596 M14597 M14598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                  NCBI
                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the yeast plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 6318)
Hartley, J.L. and Donelson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Eumycota; Ascomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           baker's yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 circular; origin of replication.
                                                                                                                                                                                                                                                                                                                                                           81012161
                                                                                                                                                                                                                                                                                                                                                                          Nature 2869 , 860-865 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces.
                                                                                                                                                                                                                                                                                                                                  gi: 4182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotations omitted.
                                         /product="protein Baker"
/translation="MNGERLLACIKQCIMQHFQPMYYDESRCVIETTRGTFPVPDNYK
/translation="MNGERLLACIKQCIMQHFQPMYYDESRCVIETTRGTFPVPDNYK
KYKTLAFAFVGHVLNTDDTPVIEKELDWPDFALVYNTIVDRIINHBELSQFISVAFIS
QLKAFIGEGLDINVKGTLWRRCKGIRRPKGVFFRYMESPFVNYKVTAFFSYLLDYKKI
ASEYHNNYKFILTFSQQAYWASGPNFSALKNVIRCSIHEYISKFVEREQDKGHIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="REP2 mRNA (major alt.)"
complement (4108..5184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4108..5195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="REP2 mRNA (major alt.)"
complement (4108..5223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4108..5183)
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DRIIGNSQRMANIKIRRTKFKSVLYHIIKELIQSQGTVKVYRGSSFSHDSIKISIHYE
                        ELPPEEDPSREINNVQHEVNSLTEQDAEADEGLWGEIDSLCEKWQSEAEDQTEAEIIA
                                                                                                                                                                                                                complement (887..2008)
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                                                                                                                                                              /codon_start=1
                                                                                                                                                                                        /note="NCBI gi: 4183"
                                                                                                                                                                                                                                      /plasmid="2 micron plasmid"
                                                                                                                                                                                                                                                              /organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="REP2 mRNA (minor alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="REP2 mRNA (major alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bound_moiety="FLP recombinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="FLP-recombinase binding site B [9]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 43;
Pred. No. 4.89e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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/note="NCBI gi: 4184" complement (4308..5198) .•

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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION Cloning vector sequence (E. coli/yeast/phage P1) ADH2 gene,
promoter; beta-lactamase gene; TRP1 gene; CYC1 gene, terminator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDOT
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Best Local Similarity 76.5%;
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                                                                                                promoter
                                                                                                                                      misc_feature
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misc_feature
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                                                                                                                                                                                                                                                                                                 Submitted (07-JUN-1993) Martin L. Pall, Department of Genetics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A series of yeast/Escherichia coli lambda expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunelli, J.P. and Pall, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brunelli, J.P. and Pall, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNECOYST
                                                                                                                                                                                                                                                                            Cell Biology, Washington State University, Pullman, WA 99164-4234,
                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                       Pall,M.L.
                                                                                                                                                                                                                                                                                                                                                                            Yeast 9, 1309-1318 (1993)
94205260
                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid excision
                                                                                                                                                                                                                                                                                                                                                                                                                                  designed for directional cloning of cDNAs and cre/lox-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94205259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A series of yeast shuttle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artificial sequences; Cloning vehicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vector DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and two replication origins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast
                                                                                                                                                                                                                                                                                                                                                          } (bases 1 to 6445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 6445)
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NGMLSSQEASQAAIDLMLQNNKLLDNRKQLYKSIAIILGRLPEKDKKRATEMLMRKMD
   /note="beta-lactamase" 2890..3790
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                                       1799..2889
                                                                            /gene="ADH2"
                                                                                                 81..668
                                                                                                                                                                               /organism="Cloning vector"
                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                  standard_name="polylinker"
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Pred. No. 4.89e-08;
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SO THE TENT OF THE ပ ₽ ORIGIN BASE COUNT Query Match Best Local S Matches LT 22 CV37458 5068 gaagttcctatactttctagagaataggaacttc 5101 misc_feature 10-NOV-1995 (Rel. 45, Last updated, Version 1)
Yeast CUP1 expression-multicopy (2micron) cloning vector YRTAG300
with the hemagglutinin tag sequence, complete sequence. selection). 10-NOV-1995 10-NOV-1995 misc_feature misc_feature rep_origin U37458; terminator source ě Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA MCBI gi: 1052969 Submitted (03-OCT-1995) to the EMBL/GenBank/DDBJ databases. Lieberman B.; Endomycetales; Saccharomycetaceae. Eukaryota; Saccharomyces cerevisiae (yeast) -6624 34 gaagttcctatacNNNNNNNngaataggaacttc 1 Similarity 76.5%; 26; /standard_name="CYC1 terminator" 1790 a 1354 c 1443 g 1858 t Plantae; Thallobionta; Eumycota; Hemiascomycetes; standard; circular DNA; FUN; 6624 BP (Rel. Conservative complement (4514..5215) 5880..6420 5785..5850 3040.. region fused in frame to a start codon and and two restriction sites (SstI and XhoI) \P 5660..5745 /product="N-(5'-phosphoribosyl)-anthranilate isomerase" /note="pid:g1052971" 574..1434 promoter, Cyc terminator and the hemagglutinin coding /organism="Saccharomyces cerevisiae"
/note="based on pRS424 (TRP selection); includes CUP1 3790..5465 transl_table=11/ /note="NCBI gi: 1052971" /gene="TRP1" /note=*HA TAG with start codon /product="beta-lactamase" transl_table=11/ /note="NCBI gi: 1052970" Location/Qualifiers /note="lox site" /note="lox site" /note="TRP1 /codon_start=1 note="pid:g1052970" codon start= 'note="2 micron origin" 45, Created) 100.0%; 3098 gene" Score 26; DB 61; Pred. No. 4.89e-08; 0; Mismatches DB 61; Length 6445; 00 (EcoRI-HATAG-SSTI-XHOI) * Indels 0; Gaps 0

Sequence 6624 BP; 1845 A; 1543 C; 1397 G; 1839 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-OCT-1995) Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U37458
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                    Similarity
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/note="based on pR3424 (TRP selection); includes CUP1
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                                                                                                                                                                                                              /product="N-(5'-phosphoribosy1)-anthranilate isomerase"
/translation="MKHTKAAWSMSVINFTGSSGPLVKVCGLQSTEAAECALDSDADL
                                                                                                                                                                                                                                                            transl_table=11
                                                                                                                                                                                                                                                                                /codon_start=|
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                                                                                                                                                                                                                                                                                                                        /gene="TRP1"
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                                                                                                                                                                                            Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning vector pRS425
                               ENTRY YEP 24
                                                                 Gilbert under the auspices of the GenBank Currator
                                                                                  These data and their annotation were supplied to GenBank by Will
                                                                                                 Unpublished
                                                                                                                      Obtained from VecBase 3.0
                                                                                                                                        Gilbert, W.
                                                                                                                                                                        Artificial sequences
                                                                                                                                                                                                            Synthetic construct DNA
                                                                                                                                                                                                                                             YEp24 yeast extrachromosomal L09156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sikorski, R.S. and Hieter, P.
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1 (bases 1 to 6849)
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             TITLE YEp24 - Yeast Extrachromosomal plasmid
                                              Yeast Extrachromosomal plasmid
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Query Match Best Local Similarity

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Score 26; DB 61; Pred. No. 4.89e-08;

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5154 gaagttcctatactttctagagaataggaacttc 5187

FEATURES

NCBI gi: 397134

S.cerevisiae/E.coli shuttle vectors'. YEAST, 7, 609-615 high copy replicative, integrative and single-stranded

source

REFERENCE REFERENCE SOURCE SDOOT May 14 13:48 REFERENCE REFERENCE KEYWORDS ACCESSION DEFINITION REFERENCE TITLE AUTHORS TITLE TITLE TITLE AUTHORS ORGANISM JOURNAL AUTHORS MEDLINE MEDLINE JOURNAL JOURNAI JOURNAL AUTHORS JOURNAL AUTHORS 26 The pFI46L was constructed from pUC19 plasmid where two alu I sites were modified. The site 629 was replaced by a BglII linker and the site 747 by a ClaI site. The yeast selectable marker has been cloned in the BglII site and the 2 micron 2.2 kb EcoRI fragment A family of low and high copy replicative, integrative and single-stranded S. cerevisiae/E. coli shuttle vectors Yanisch-Perron,C., Vieira,J. and Messing,J.
Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors
Gene 33 (1), 103-119 (1985) cloning vectors multicopy Saccharomyces cerevisiae/E. coli shuttle vector. containing ORI and STB gene has been cloned at the ClaI site. The pFLA6L is described in Bonneaud et al (1991): 'A family of low and Yeast 7 (6), 609-615 (1991) Minvielle-Sebastia, L. and Lacroute, F. Bonneaud, N., Ozier-Kalogeropoullos O., CGM, CNRS, 91190 Gif sur Yvette, France e-mail:odile%FRCGM51.BITNET@vm.gmd.de Submitted (01-JUN-1993) to the EMBL/GenBank/DDBJ databases Direct Submission Ozier-Kalogeropoullos,O. Chevalier, M.R. and Lacroute, F.
Trancriptional and traductional expression of a chimeric Proc. Natl. Acad. Sci. U.S.A. 76 (3), 1035-1039 (1979) hybrid DNA molecules High-frequency transformation of yeast: autonomous replication of Struhl, K., Stinchcomb, D.T., Scherer, S. and Davis, R.W. 85180545 artificial sequence; cloning vectors.

1 (bases 1 to 644; 3499 to 3625; 5877 to 7822) cloning vectors. pUC19 plasmid. 2-micron yeast replication origin; LEU2 selectable marker; X70269 CVPFL46L Gene 1, 11-19 (1980) bacterial- yeast plasmid 79180126 (bases 1 to 7822) (bases 3625 to 5877) (bases 644 to 3499) (bases 1 to 7822) Ozier-Kalogeropoulos, O., Li, G.Y., Labouesse, M., 7822 bp in yeast FI.P rge 15-AUG-1995

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Sequence 7834 BP; 2192 A; 1672 C; 1646 G; 2324 T; 0 other;
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Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
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Colicelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-AUG-1995) to the EMBL/GenBank/DDBJ databases.
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Colicelli,J., Birchmeier,C., Michaeli,T., O'Neill,K., Riggs,M.
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Sequence 4 from patent US 5434073. I13185
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A19996 standard; DNA; SYN; 7859 BP.
A19996;
14-UUL-1995 (Rel. 44, Created)
14-UUL-1995 (Rel. 44, Last updated, Version 1)
SEQ ID NO: 4; Synthetic plasmid pSW6.
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Patent number WO9109125-A/4, 27-JUN-1991.
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                                                                                                                     unidentified
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BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other;
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Cloning vector pACT2 MatchmakerII, complete sequence.
                                                                                                                                                                                                                                                                                                              3 or E-mail TECH@CLONTECH.COM.
                                                                                                                                                                                                                                                                                                                               an error in this sequence, please contact CIONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extens.
                                                                                                                                                                                                                                                                                                                                                                                          customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fabian Way, Palo Alto, CA 94303, USA. To place an order cal. (415) 424-8222 or (800) 662-2566, extension 1. International
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-JUN-1995) John S. Stile, Clontech Laboratories, Inc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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YANLRP CNFASDS LLDLSP IKPQFAKGTDFVVVRELVGG I YFGKRKEDDGDGVAMDSE
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/QHQLIDSAAMILVKNPTHLNGIIITSNMFGDIISDEASVIPGSLGLLPSASLASLPD

-10_signal -35_signal BASE COUNT 2 S 망 Query Match 100.0%; Best Local Similarity 76.5%; Matches *CLONTECH Vectors On Disk, version 1.3*; Cloning 12-0CT-1995 12-0CT-1995 030497; CV30497 cgs promoter SG misc_feature terminator misc_feature Unpublished. Cloning vector pAS2-1 rep_origin Artificial sequences; Cloning 1-8393 1-8393 584 gaagttcctattctctagaaagtataggaacttc 617 34 gaagttcctattcNNNNNNNgtataggaacttc 34 vector pAS2-1, 26; 2423 standard; circular DNA; SYN; 8393 BP (Rel. 45, (Rel. Conservative ω /product="beta-lactamase"
/translation="MSIGHFRVALFFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
/translation="MSIGHFRVALFFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILESFRPEERFPMMSTFKVLLGGAVLSRVDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELGSAAITMSDNTAANILLITIGEPKELTAFLHMMGDHVTRL
DRWEPELMEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGPL 8029..>8034 8052..8057 EIGASLIKHW" polypeptide; stop codon is located downstream within the multiple cloning site; NCBI gi: 915411" complement(<5081.5488)
/note="encodes 5' region of the Gal 4 activation domain</pre> /note="NCBI gi: 915412" complement (7127.. 6336..6979 5504..5901 AFGITTGMFNTTTMDDVYNYLFDDEDTPPNPKKE" NGPNLITTQTNSQALSQPIASSNVHDNFMNEITASKIDDGNNSKPLSPGWTDQTAYN /transl_table=11
/product="Gal 4 activation domain polypeptide"
/translation="MDKAELIPEPPKKKRKVELGTAANFNQSGNIADSSLSFTFTNSS 5042..5068 4415..4742 group(4268..4327,4367..4412) AGIRTGDLGGSNSTTEVGDAVAEEVKKILA" KNTAFGLYEPCHGSAPDLPKNKVDPIATILSAAMMLKLSLNLPEEGKAIEDAVKKVLD LRSALPAGWF IADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA transl_table=11 /codon_start= /note="pBR322 origin of replication" /note="S. cerevisiae ADH1 Promoter" /codon_start=1 /note="encodes HA epitope which fuses to Gal 4" /note="S /note="Lox Sites" 45, 1677 c Created) Last updated, Version 1) complete sequence. cerevisiae ADH1 terminator" 1757 Score 26; DB 61; Pred. No. 4.89e-08; **.**; vectors. Mismatches φ 2260 Length 8117; Indels 0 Gaps 0

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T FIF FΤ S S S published literature and other sources, together with partial sequences obtained by CLONTECH. If you suspect there is an error this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or rep_origin misc_feature misc_feature misc_feature promoter SG This vector can be obtained from CLONTECH Laboratories, Inc., 4030 Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, Sequence 8393 BP; terminator source Key please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence Alto, CA 94303, USA Submitted (28-JUN-1995) to the EMBL/GenBank/DDBJ databases. John S. Stile, CLONTECH Laboratories, Inc., 4030 Fabian Way, rep_origin rep_origin E-mail TECH@CLONTECH.COM. NCBI gi: 988208 has been compiled from information in the sequence databases and 3" 5971..6016 5953..5970 /transl_table=11
/product="fusion protein"
/note="pid:g988211" /transl_table=11 /note="pid:g988212" complement (7403..8263) /note="pUC origin of replication" 6232..7403 6032..6224 5502..5942 monoclonal antibody binding; 4768..5475 complement (4018..4305) Location/Qualifiers /codon_start=] /note="NCBI gi: 988212" /gene="ampicillin resistance" /note="from ADH1 gene; contains stop codons for frame /note="encodes epitope for monoclonals Dll and F10 binding /note="contains Gal4 binding domain and epitopes for monoclonal antibody binding; NCBI gi: 988211" 5502..6065 /note="pid:g988210" transl_table=11/ /note="f1+ origin" 2609..327 /note="pid:g988209" transl_table=11/ 1..1348 /note="multiple cloning site" note="from ADH1 gene" 'gene="CYH2" codon_start= 'gene="TRP1" 1884..2558 note="two micron origin of replication organism="Cloning vector pAS2-1" note="encodes Gal4 binding domain" codon_start=1 codon_start=1 note="NCBI gi: 988210" note="NCBI gi: 988209" 2351 A; 1754 C; 1871 G; 2416 T; 1 other; (B form)" Palo 4030 in 1,2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUN-1995) John S. Stile, CLONTECH Laboratories, Inc., 4030 Fabian Way, Palo Alto, CA 94303, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONTECH Vectors On Disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kitts, P.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               partial sequences obtained by CLONTECH. If you suspect there is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This vector can be obtained from CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-mail TECH@CLONTECH.COM.
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ESNQEYQEF LGLPV I KRLVFPKDCN I LLSAASQKPHSF I PLFDSEAGGTGELLDNNS I
MDKYHPGYFGKXWYEILPQATSSFLEASLELGQIVDIDPRRQERPILEICF*
                                   transl_table=11
                                                                                                                                complement (4018..4305)
                                                                                                                                                         /note="fl+ origin"
                                                                                                                                                                                2609..3277
                                                                                                                                                                                                       VKNAKK.
                                                                                                                                                                                                                              SDWVGRQESPESLHFMLAGGLTPENVGDALRLNGVIGVDVSGGVETNGVKDSNKIANF
                                                                                                                                                                                                                                                                                                                                                                                  /gene="TRP1"
                                                                 /codon_start=1
                                                                                    /note="NCBI gi: 988210"
                                                                                                           /gene="CYH2"
                                                                                                                                                                                                                                                                                                translation="MSVINFTGSSGPLVKVCGLQSTEAAECALDSDADLLGIICVPNR/
                                                                                                                                                                                                                                                                                                                     transi_table=11/
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                                                                                                                                                                                                                                                                                                                                                                 /note="NCBI gi: 988209"
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                       translation="MPSRFTKTRKHRGHVSAGKGRIGKHRKHPGGRGMAGGQHHHRIN/
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                                                                                                                                                                           Cloning vector YEp213. Cloning vector YEp213
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Stillman, D.J.
                                                       Meth. Enzymol. 185, 234-279 (1990)
                                                                           based vectors
                                                                                              Propagation and expression of cloned
                                                                                                                  Rose, A.B. and Broach, J.R.
                                                                                                                                    Artificial sequences; Cloning vector 1 (bases 1 to 10667)
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/transl_table=11
/translation="MSIQHERVALIPEFRAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="NCBI gi: 988212"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="encodes epitope for monoclonals D11 and F10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ampicillin resistance"
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FEATURES COMMENT

NCBI gi: 416341

Location/Qualifiers

...10667

source

BASE COUNT

2837

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/organism="Cloning vector YEp213" 2459 c 2350 g 3021 t

/lab_host="Saccharomyces cerevisiae"

Query Match 100.0%; Best Local Similarity 76.5%;

Score 26; DB 61; Length 10667; Pred. No. 4.89e-08;

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Conservative

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Mismatches

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and Molecular Biology, University of Utah Medical Center, City, UT 84132 USA

Salt Lake

Submitted (16-NOV-1993) David J. Stillman, Dept. of Cellular, Viral

May 14 13:48

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MEDLINE REFERENCE AUTHORS ငှ 맑 BASE COUNT REFERENCE REFERENCE SOURCE KEYWORDS ORIGIN BASE COUNT COMMENT FEATURES COMMENT ACCESSION DEFINITION rocas RESULT FEATURES REFERENCE JOURNAL MEDLINE TITLE TITLE ORGANISM Matches Query Match 84.6%; Best Local Similarity 70.6%; MEDLINE TITLE Query Match JOURNAL AUTHORS AUTHORS JOURNAL AUTHORS ORGANISM source source 90 gaagttcctattctctagaaagtataggaacttc 123 34 gaagttcctatacNNNNNNNnnnnnngaataggaacttc 1 39 Cloning vector pRS424 Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake City, UT 84132 USA Multifunctional yeast high-copy-number shuttle vectors Gene 110 (1), 119-122 (1992) Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989) A system of shuttle vectors and yeast host strains designed 003453 57 a 47 c 46 g 103 bp upstream of XbaI site. [1] examines whether cleavage sites are specific when the DNA-associated protein is stripped away and draws the conclusion that the specificity of DNAase I is dependent on the presence of NCBI gi: 416324 Direct Submission Stillman, D.J. Sikorski, R.S. and Hieter, P. artificial sequence; cloning vectors. Cloning vector pRS424 PRS424 5616 bp DNA circular SYN 24-MAY-1995 Yeast episomal vector pRS424 with TRP1 marker, complete sequence. NCBI gi: 172188 nucleoprotein. 8413864 J. Mol. Biol. 173, 1-13 (1984) plasmid DNA chromosome Fagrelius, T.J. and Livingston, D.M. Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Endomycetales; Saccharomyces cerevisiae 92184105 Hieter,P. 89276910 Location of DNAase I sensitive cleavage sites in the yeast 2 mu-m Saccharomycetaceae. 24; (bases 1 to 5616) (bases 1 to 5616) (bases 1 to 5616) (bases 1 to 200) 1513 Conservative စ /organism="cloning vector pRS424" 1221 c 1356 g 1526 t Location/Qualifiers 1..5616 /organism="Saccharomyces cerevisiae" a 47 c 46 g 50 t Location/Qualifiers 84 . 64: Score 22; DB 43; Pred. No. 1.34e-04; Score 0; Mismatches g 22; DB 61; ; 10; Length 5616; Length Indels <u>;</u> Gaps <u>,</u>

RESULT LOCUS

37

KEYWORDS

U03498

Yeast YEP13

10667 bp DNA episomal vector YEp13,

complete sequence circular SYN

17-NOV-1993

SOURCE ACCESSION DEFINITION

ORGANISM

Cloning vector YEp13 Cloning vector YEp13.

REFERENCE

Artificial sequences; Cloning vector. 1 (bases 1 to 10667)

TITLE

Propagation and expression of cloned

genes in yeast: 2-umcircle

Rose, A.B. and Broach, J.R.

AUTHORS

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9951 gaagttcctatactttctagagaataggaacttc 9984

34 gaagttcctatacNNNNNNNngaataggaacttc 1

Pocas DEFINITION SOURCE ACCESSION 38 K01710 YSCPL2M 200 bp Yeast (S.cerevisiae) plasmid.
Yeast (Saccharomyces cerevisiae) 2 region. 200 2 micron plasmid DNA micron plasmid DNA (A-form) MId inverted repeat 10-DEC-1984

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9951 gaagttcctatactttctagagaataggaacttc 9984

34 gaagttcctatacNNNNNNNgaataggaacttc 1

ORIGIN

Query Match 100.0%; Best Local Similarity 76.5%;

Score 26; DB 61; Pred. No. 4.89e-08;

DB 61; Length 10667;

Matches

26;

Conservative

.

Mismatches

8

Indels

9

Gaps

0

BASE COUNT

2889

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/organism="Cloning vector YEp13" 2443 c 2366 g 2969 t

/lab_host="Saccharomyces cerevisiae"

Location/Qualifiers
1..10667

FEATURES COMMENT

> NCBI gi: 416340 City, UT 84132 USA

source

REFERENCE

Meth.

Enzymol. 185, 234-279 (1990)

90340124 based vectors

(bases 1 to 10667)

JOURNAL AUTHORS MEDLINE JOURNAL

> Direct Submission Stillman, D.J.

Submitted (16-NOV-1993) David J. Stillman, Dept. of Cellular, Viral

and Molecular Biology, University of Utah Medical Center, Salt Lake

Matches

24;

Conservative

ç

Mismatches

10;

Indels

0

Gaps

0

Best Local Similarity 70.6%;

Pred. No. 1.34e-04;

May 14 13:48

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                        LT 42
CV37458
U37458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6070 gaagttcctattctctagaaagtataggaacttc 6103
                                    NCBI gi: 1052969
                                                       Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                           10-NOV-1995 (Rel. 45, Created)
10-NOV-1995 (Rel. 45, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                               Submitted (03-0CT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          Eukaryota; Plantae; Thallobionta; Eumycota; Hemiascomycetes;
                                                                                                                                                                                                                                               Saccharomyces cerevisiae (yeast)
                                                                                                                                                                                                                                                                                       with the hemagglutinin tag sequence,
                                                                                                                                                                                                                                                                                                          Yeast CUP1 expression-multicopy (2micron) cloning vector YRTAG300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                         Endomycetales; Saccharomycetaceae
                                                                                                                                           Lieberman B.;
                                                                                                                                                                -6624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 gaagttcctatacNNNNNNNgaataggaacttc 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1845
                                                                                                                                                                                                                                                                                                                                                                                           standard; circular DNA; FUN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt GELLDWNSISDWVGRQESPESLHEMLAGGLTPENVGDALRLNGVIGVDVSGGVETNGVKDSNKIANFVKNAKK"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4514..5215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LG I I CVPNRKRT I DPV I ARK I SS LVKA YKNSSGTPKY LVGVFRNOPKEDVLALVNDYG
ID I VOLHGDESWOE Y QEFLGLPV IKR LVFPKDCN I LLSAASOKPHSF I PLFDSEAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IELDINSGKILESERPEERFPMMSTEKVILCGAVISRIDAGGEGLGRRIHYSQNDIVE
YSPVTEKHITDGMTVREICSAAITMSDNTAANLLITTIGGEKELTAFIHMMGDHVTRI
DRMEPEINEAIPNDERDTTMPVAMATTIRKILTGELITIASRQQIIDMMEADKVAGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region fused in frame to a start codon and and two restriction sites (SstI and XhoI)"
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MKHTKAAWSMSVINFTGSSGPLVKVCGLQSTEAAECALDSDADL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="NCBI gi: 1052971"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="HA TAG with start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3040..3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574..1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter, Cyc terminator and the hemagglutinin coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="based on pRS424 (TRP selection); includes CUP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="N-(5'-phosphoribosyl)-anthranilate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="TRP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRSALPAGWF IADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="NCBI gi: 1052970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1543 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1397 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 84;
Pred. No. 1.34e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 10;
                                                                                                                                                                                                                                                                                       complete sequence. selection).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1839 t
                                                                                                                                                                                                                                                                                                                                                                                               6624 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EcoRI-HATAG-SSTI-XHOI) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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LOCUS
DEFINITION
ACCESSION င့ 밁 DT PH RAN OCC STATE Ş 밁 T T T BASE COUNT REFERENCE SOURCE KEYWORDS May 14 13:48 COMMENT FEATURES TITLE ORGANISM Matches Query Match 84.6%; Best Local Similarity 70.6%; Matches Query Match 84.6%; Best Local Similarity 70.6%; JOURNAL AUTHORS LT 44 A19996 3131 gaagtteetattetetagaaagtataggaaette 3164 None source /organism="Artificial sequences" Sequence 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other; source "PROTEINS AND NUCLEIC ACIDS";
Patent number W09109125-A/4, 27-JUN-1991. 5763 gaagtteetataetttetagagaataggaaette 5796 /gene="ADH1" Sequence 7834 BP; 2192 A; 1672 C; 1646 G; 2324 T; 0 other; SEQ ID NO: 4; Synthetic plasmid pSW6. 14-JUL-1995 (Rel. 44, Created)
14-JUL-1995 (Rel. 44, Last updated, Version 1) A19996; promoter terminator Artificial sequences 34 gaagttcctatacNNNNNNNgaataggaacttc 1 1 gaagttcctattcNNNNNNNgtataggaacttc 45 = = = = = unidentified Patent: WO 9207874-A 33 14-MAY-1992; yeast expression vector pSW6 seq A18079 NCBI gi: 513171 AN INTEGRINAFFINITY SEQUENCE PHARMACEUTICALLY ACTIVE PROTEINS COMPRISING AN ACTIVE PROTEIN AND 1 (bases 1 to 7984) unclassified unidentified A18079 24; 24; 2345 a standard; DNA; Conservative Conservative 1..7984 /gene="ADH1" 6381..7834 /organism="Artificial sequences" /lab_host="yeast expression vector pSW6" ₁ 1695 c 1638 g 2306 t 1..7859 Location/Qualifiers /note="polylinker"
39..505 Location/Qualifiers 7984 bp ;NYS Score 22; DB 15; Pred. No. 1.34e-04; Score 22; DB 88; Pred. No. 1.34e-04; 0; 0; Mismatches 10; 7859 BP DNA Mismatches 10; FIPige 34 Ĭ <u>₹</u> Length 7834; Length 7859; Indels Indels 0 0; Gaps Gaps 0 0;

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ORIGIN

Query Match 84.6%; Score 22; DB 34; Length 7984;
Best Local Similarity 70.6%; Pred. No. 1.34e-04;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Search completed: Tue May 14 13:58:25 1996 Job time : 534 secs.

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FLP mg

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on:

Tue May 14 13:58:43 1996; MasPar time 4.93 Seconds 458.714 Million cell updates/sec

Tabular output not generated.

Perfect Score: Description: (1-34) from frt.seq 26

N.A. Sequence: Comp: 1 gaagttcctattcNNNNNNNgtataggaacttc 34 cttcaaggataagNNNNNNNNcatatccttgaag

Scoring table: TABLE default Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 84802 seqs, 33246950 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

n-geneseq22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16

Statistics: Mean 5.329; Variance 3.136; scale 1.699

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•*				
Result No.	Score	Query Match	Query Match Length DB ID	B ID	Description	Pred. No.
2	26	100.0	54 12	2 067140) Complete FRT site lac	5.30e-06
2	26	100.0	1340 19	-	_	5.30e-06
ω	26	100.0	7859	7 044265	pSW6 for expression o	5.30e-06
4	26	100.0	7859	2 012154	Shuttle vector pSW6.	5.30e-06
5	26	100.0	7984	4 025185	pSW6 expression vecto	5.30e-06
6	25	96.2	33	5 029100	Sequence of FLP recom	2.13e-05
c 7	24	92.3		2 067141	Partial FRT site lack	8.46e-05
∞	22	84.6	54 12		_	1.28e-03
c 9	22	84.6		_	•	1.28e-03

	000 0 00000 0 00000
	10 11 11 11 11 11 11 11 11 11 11 11 11 1
	22 22 22 22 22 22 20 20 20 20 20 20 20 2
	84.6 84.6 84.6 661.5 577.7 76.9 86.6 661.5 577.7 757.7
	1340 7859 7989 7989 7984 33 41 4093 4093 42 1047 1971 1971 3249 3400 42 1047 1971 501 501 501 501 501 501 501 501 501 50
	110 110 110 110 110 110 110 110 110
ALI GNMENTS	Q93078 Q12154 Q12155 Q251165 Q251166 Q51746 Q851746 Q817141 Q67134 Q67134 Q671367 Q71789 Q71789 Q71789 Q39050 Q81164 Q89060 Q8164 Q89060 Q81650 Q8165
	Neomycin-resistance c Shuttle vector pSW6. pSW6 for expression vecto Sequence of FIP recom Partial FRT site lack Oligonucleotide probe Base substituted E.co ced-4. DNA primer used for c Human Natriuretic Pep cDNA encoding recepto E.coli/S.cerevisiae s Pre-pro-cobra C3 codi K.lactis/S. cerevisiae s Pre-pro-cobra C3 codi K.lactis/S. cerevisiae s E.coli/S.cerevisiae s E.coli/S.cerevisiae s E.coli/S.cerevisiae s Encoding new Sequence encodi
	1.28e-03 1.28e-03 1.28e-03 1.28e-03 1.89e-03 1.83e-02 2.91e+00 2.91e+00 9.70e+00 9.70e+00 9.70e+00 9.70e+00 9.70e+00 1.313e+01 3.13e+01

Complete FRT site lacking additional 5 FLP binding sites.
Maize; Zea mays; cereal; grass; protoplast; FLP; ss.
DNA constructs - for creating transgenic eukaryotic cells
Disclosure; Page 51 79pp; English.
This sequence is of the complete FRT site which is ligated into the
BglIII site of the ubiqutin first exon. This FRP site lacks
additional 5 FLP protein binding sites, and has application in the
construction of transgenic eukaryotic cells.
54 BP; 18 A; 9 C; 11 G; 16 T;
additional 5 FLP binding sites. rass; protoplast; FLP; ss. ing transgenic eukaryotic cells English. English. English Trist ewhich is ligate in first exon. This FRP site lainding sites, and has application eukaryotic cells. 9 C; 11 G; 16 T; Score 26; DB 12; Length 54;

Best Local Similarity 76.5%; Pred. No. 5.30e-06;

Matches

26;

Conservative

0;

Mismatches

8

Indels

0; Gaps

0

င့ 맑 Q93078 misc feature enhancer misc_feature misc feature allograft rejection; Gal epitope; gene disruption; mouse; hyperacute rejection; xerotransplantation; donor organ; Alpha-1, 3-galactosyltransferase; alpha-1, 3-GalT; transgenic animal; Neomycin-resistance cassette. 093078; misc feature promoter Not specified. homologous recombination; knock-out; neomycin-resistance; recombination as a means of suppressing the GAL epitope. Sequence 1340 BP; 285 A; 362 C; 391 G; 302 T; development of a DNA construct (pNeo-alpha-GT10.8B) The neomycin-resistance cassette given in Q93078 was used in the Disclosure; Fig.16a-16b; 184pp; English. transplants transferase gene; for eliminating hyperacute region in human New alpha-1,3-galactosyltransferase and leukaemia inhibitor factor MPI; 95-275446/36. Robbins AJ, Crawford RJ, (SVIN-) ST VINCENT'S HOSPITAL MELBOURNE LTD. 27-JAN-1994; US-188607. 26-JAN-1995; US-188607. 27-JAN-1995; IB0088 03-AUG-1995. WO9520661-A1. /*tag= /function= FLP polyA signal /function= herpes simplex virus polyA_signal /product= /*tag= function= herpes simplex virus /*tag= d promoter /function= polyoma virus enhancer repeats /*tag= function= FLP /#tag= function= linker sequence 10-DEC-1995 interrupt the mouse alpha-1,3-GalT gene by means of homologous corresp. DNA and nucleic acid constructs for inactivating the function= linker sequences /*tag= /*tag= 34 6 gaagttoctatactttctagagaataggaacttc gaagttcctatacNNNNNNNngaataggaacttc 1 standard; е neomycin-phosphotransferase (first entry) Dapice AJF, recombinase target site recombinase target Location/Qualifiers 1..28 1250..1310 1189..1249 385..1188 250..385 105..249 29..104 1311..1340 CDNA; 1340 BP Pearse MJ, tyrosine-kinase tyrosine-kinase site Rathjen PD; 39 used to

May 14 13:50 FLP:mg

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S В 2 S 2 2 2 2 2 3 5 S В Query Match 100.0%; Best Local Similarity 76.5%; Query Match Matches Matches Best Local Similarity LT 3 Q44265 Synthetic. W09109125-A. Q12154 , Q12154; 3131 gaagttcctattctctagaaagtataggaacttc 3164 Q44265;
23-NOV-1993 (first entry)
pSW6 for expression of LD78 synthetic gene.
SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha; Fusion protein; blood clotting; coagulation; antithrombotic; thrombolysis; streptokinase; Shuttle vector pSW6. Sequence S. cerevisiae. used to direct export of the LD78 protein. The yeast expressivector pSW6 (NCIMB 40326) is based on the 2 micron circle from 23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587. /*tag= circular; ds macrophage inflammatory protein; multimer; tumour therapy; psoriasis; hyperproliferation; yeast expression vector; The secretion signals from the yeast mating type factor alpha were Secretion aids purification and rapid analysis of LD/8. An expression vector was designed to enable secretion of LD78 Disclosure; Page 159-168; 294pp; English providing better tissue penetration alpha - unable to form stable multimer higher than dodecamer, Protein with stem cell inhibition activity, e.g. LD78 or MlP-1 WPI; 93-227322/28. Hunter MG; Craig S, (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Craig S, Czaplewski LG, Edwards RM, 08-JUL-1993. W09313206-A. /note= "base illegible in the specification" misc_difference 1773 Saccharomyces cerevisiae 17-SEP-1991 (first entry) the extracellular medium after expression in S. cerevisiae. 48 gaagtteetattetetagaaagtataggaaette 81 1 gaagttcctattcNNNNNNNngtataggaacttc 34 gaagttcctattcNNNNNNNngtataggaacttc 34 standard; DNA; standard; 26; 26; 7859 BP; Conservative Conservative DNA; Location/Qualifiers 100.0%; 7859 7859 BP 2317 A; ₽ Pred. No. 5.30e-06, Score 26; DB 15; Pred. No. 5.30e-06; Score 26; 0 0; Mismatches Mismatches 1667 C; DB 7; Gilbert RJ; The yeast expression 1585 G; plasmid; fibrinolysis; 00 Length 7859; .. Length 1340; Indels circular; 2289 T; <u>.</u> <u>.</u>. 6 Gaps Gaps 88. 0 0,

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S 밁 Query Match 100.0%; Best Local Similarity 76.5%; Matches Q25185; 3131 gaagttcctattctctagaaagtataggaacttc 3164 vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of visiae and contains origins of replication for both, the leu2 gene (selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli ColEl-based replicon pAT153. The 07-DEC-1989; GB-027722. 07-DEC-1990; WO-G01911. gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide this fusion is under control of a galactodse regulated promoter which contains hybrid DNA from S. cerevisiae GAL 1-10 promoter and prophylaxis. Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and Dawson KM, Hunter MG, Czapleswski LG, 07-DEC-1990; 23-OCT-1991; G01860. 24-OCT-1990; GB-023149. Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; pSW6 expression vector. Q25185 See also Q12153-Q12156, Q12158-Q12162 and Q12490. Sequence 7859 BP; 2317 A; 1656 C; 1600 occurring are released specifically at the place where clot formation is are present at the site of the target thrombus so the active agents thrombotic activity. can be cleaved, releasing the individual proteins which have antipression vectors in which the hirudin gene is linked to a second in E. coli K12 Hw87. mid was used for the expression of a synthetic hirudin HV-1 gene gene can be excised by digestion with HindIII and BamHI. The plasthe S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF shuttle vector capable of replcation in both E. coli and S. ceredeposited in S. cerevisiae strain BJ2168 as NCIMB 40326. The vector is based on the 2u circle from S. cerevisiae. Disclosure; Page 71; 115pp; English WPI; 91-208151/28 (BRBI-) BRIT BIO-TECHN LTD. New proteins comprising active protein and integrin-affinity WPI; 92-183627/22. Dawson KM, Edwards RM, Fallon A; WO9207874-A. phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss. ampicilin resistant locus; epidermal growth factor; GAL 1-10; (BRBI-) BRITISH BIO-TECHNOLOGY LTD. 14-MAY-1992. Saccharomyces cerevisae. 18-NOV-1992 (first entry) link contains a cleavage site for e.g. factor X or thrombin which 1 gaagttcctattcNNNNNNNgtataggaacttc 34 standard; DNA; 7984 are antithrombotics useful in treating and preventing G01911. Conservative The enzymes which cleave the fusion protein The plasmid can be used to construct ex-ВÞ Pred. No. 5.30e-06, Score 26; DB 2; 0, Mismatches 1600 Length 7859; ... Indels ç 2286 T; It is a 0; Gaps 0

May 14 13:50 FLP mg

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Ş 뮹 Matches Query Match Best Local Similarity 76.5%; 3131 gaagttcctattctctagaaagtataggaacttc 3164 cerevisae phosphoglycerate kinase (PGK) promoter. the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. Disclosure; Page 67; Ogorman SV, Wahl GM; WPI; 92-331739/40. 08-MAR-1991; US-666252. 06-MAR-1992; U01899. W09215694-A. /*tag= misc feature gene inactivation; ss. FLP recombinase; site-specific integration system; gene activation; Sequence of FLP recombination target site Q29100; Q29100 standard; DNA; 33 BP Sequence site-alpha-factor adapter-gene-BamHI site. expression vector must therefore have the general composition: HindIII the alpha-factor pro-peptide. Genes to be inserted into the pSW6 gene in pSW6 can be removed by digestion with HindIII and BamHI. terminated in this vector by the natural yeast PGK terminator. epidermal growth factor (EGF). The expression of this fusion is under contains contains an alpha- factor pre-pro peptide fused in-frame to this greatly facilitates genetic manipulation with this vector. coli. This vector has enhanced ability for passage through amipicillin resistant locus for selection of plasmid maintenance in E. also contains the leu2 gene (a yeast selectable marker) and the coli as it contains the origin of replication for both organisms. It vector capable of replication in both S. cerevisae and Escherichia on the 2 micron circle from Saccharomyces cerevisae. The sequence given is the yeast expression vector pSW6. myocardial infarction, stroke, nucleotides in The inventors claim a mammalian recombination system in which the FLP recombinate is pref. Q29101. The FLP recombination target site number of the 2-mu plasmid of S. cerevisiae during DNA replication. recombination reaction that is involved in amplifying the copy FLP recombinase is a protein which catalyses a site-specific Claim 33; Page 40; 49pp; English. precise modification by recombination and can be used to alter FLP-mediated gene modification in mammalian cells - giving 17-SEP-1992. Synthetic. 25-FEB-1992 removes DNA encoding both EGF and 5 amino acids from the C-terminus of repeats, (FRT) has been identified as minimally comprising two 13 base-pair ransgenes for therapeutic purposes and analysis of development (SALK) SALK INST BIOLOGICAL STUDIES 'label= spacer gaagttcctattcNNNNNNNngtataggaacttc 34 26; separated by an 8 base-pair spacer (see Q29100). The 7984 BP; Conservative (first entry) the Location/Qualifiers 14..21 spacer region 100.0%; 2348 A; Pred. Score 26; <u>,</u>. pulmonary embolism Mismatches can be No. 5.30e-06; 1698 C; DB 4; replaced with any other 1635 8 Length 7984; ç and deep vein Indels Transcription is It is a shuttle It is based <u>.</u>. E.coli and Gaps The EGF 0

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RESULT RESULT ON ACCOUNT OF THE PROPERTY OF TH င့ 밁 Š 맑 2222 Matches Query Match Matches Query Match BgIIII site of the ubiquin first exon. This FRP site lacks additional 5 FLP protein binding sites, and has application in the construction of transgenic eukaryotic cells. Sequence 41 BP; 13 A; 7 C; 8 G; 13 T; are separated by 8 nucleotides. NB, in the claims the sequence the FRT has only 12 base pairs on the 3^\prime end of the spacer. The DNA constructs - for creating transgenic eukaryotic cells
Disclosure; Page 51 79pp; English.
This sequence is of the complete FRT site which is ligated into the Q67140 standard; DNA constructs - for creating transgenic eukaryotic cells Disclosure; Page 51 79pp; English.
This sequence is of the partial FRT site which is ligated into the 04-AUG-1994. W09417176-A. Maize; Zea mays; cereal; grass; protoplast; FLP; ss. Partial 067141 Q67141 standard; apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; combination of nucleotides so long Hodges TK, 27-JAN-1994; U00927. 04-AUG-1994. W09417176-A. Synthetic. Maize; Zea mays; cereal; grass; protoplast; FLP; ss. Complete FRT site lacking additional 5 FLP binding sites. 22-MAR-1995 Q67140; WPI; 94-264090/32. Hodges TK, 29-JAN-1993; US-010997. 27-JAN-1994; U00927 Synthetic. 22-MAR-1995 MPI; 94-264090/32. (PURD) PURDUE RES FOUND. 29-JAN-1993; US-010997. (PURD) PURDUE RES FOUND. Local Similarity hes 24; Conser Local 32 agttcctatactttctagagaataggaacttc 36 gaagttcctattcNNNNNNNgtataggaactt 33 gaagttoctattototagaaagtataggaactt 33 agttcctatacNNNNNNNNgaataggaacttc 1 site FRT site lacking additional 5 FLP binding sites. Similarity 25; Lyznik LA; of the Lyznik LA; (first entry) Conservative Conservative (first entry) DNA; DNA; 92.3%; 75.0%; 96.2**%**; ubiqutin first exon. 54 41 ВP 뫈 Score 25; DB 5; L Pred. No. 2.13e-05; Score 24; DB 12; Pred. No. 8.46e-05; 0; 0; Mismatches Mismatches as the two 13 base-pair repeats, in the claims the sequence of 6 G; This FRP 11 T; œ Length Length 41; site Indels Indels 33; 0; 0. Gaps Gaps <u>.</u> <u>.</u>.

RESULT
ID 055
AC Ş 888 May 14 13:50 £ 밁 Matches Matches Query Match Query Match Best Local Best 24-MAY-1993; 108325. 26-MAY-1992; US-889651. (BECT) BECTON DICKINSON CO be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T; Q51746; construction of transgenic eukaryotic cells. Sequence 54 BP; 18 A; 9 C; 11 G; Q93078 standard; cDNA; 1340 BP WPI; 93-378844/48. 01-DEC-1993. EP-571911-A. Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; Oligonucleotide probe MK14-A Q51746 standard; additional 5 FLP protein binding sites, and has misc_feature misc_feature allograft rejection; Gal epitope; gene disruption; mouse; hyperacute rejection; xerotransplantation; donor organ; Alpha-1,3-galactosyltransferase; alpha-1,3-GalT; transgenic animal; Neomycin-resistance cassette. Q93078; cross reacted to a few non-mycobacterial spp. Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Claim 3; Page 14; 23pp; English. samples New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in Shank DD, Synthetic. 31-MAY-1994 /function= linker sequence Not specified homologous recombination; knock-out; neomycin-resistance; ss. 10-DEC-1995 (first entry) (Q51735). It hybridized to all spp. of mycobacteria tested, /*tag= 19 vhvvshhhsvhhvvhhvhvsvvvvhhvvhhvv 52 Local 34 6 gaagttcctatactttctagagaataggaacttc gaagttcctatacNNNNNNNngaataggaacttc 1 :: gaagttcctattcNNNNNNNngtataggaacttc h 84.6%; Similarity 70.6%; Similarity 24; ç Spears PA; Conservative Conservative (first entry) 29..104 Location/Qualifiers
1..28 cDNA; 84.6%; 91 Score 22; DB 9; Le Pred. No. 1.28e-03; 24; Mismatches 10; Pred. Score 0; Mismatches 9 C; 22; DB 12; No. 1.28e-03; FLP.mg ည 10; ; 10 Length 91; 16 The probe may Length 54; application Indels 7 Indels <u>,</u> 0 ij for Gaps Gaps the 0 9

/*tag=

promoter

function= *tag= function=

polyoma virus enhancer repeats 250..385

a

enhancer

FLP

recombinase target site

105..249

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RESULT
ID Q1
AC Q1
DT 17
DE Sh
KW Fu
KW an
OS Sy
PN WO
PD 27
PD 27
PR 07
PR 07 မှ 밁 Matches Query Match Best Local Similarity 70.6%; 27-JUN-1991. 07-DEC-1990; G01911. 07-DEC-1989; GB-02772 07-DEC-1990; WO-G0191 Q12154 ; Q12154; Synthetic. Fusion protein; blood clotting; coagulation; fibrinolysis; /*tag= antithrombotic; thrombolysis; streptokinase; plasmid; circular; ss. Shuttle vector pSW6. Disclosure; Fig.16a-16b; 184pp; English. transplants transferase gene; for eliminating hyperacute region in human New alpha-1,3-galactosyltransferase and leukaemia inhibitor factor corresp. DNA and nucleic acid constructs for inactivating the Robbins AJ; Crawford RJ, 27-JAN-1994; US-188607. 26-JAN-1995; US-188607. misc_feature misc_feature polyA signal /*tag= promoter WO9109125-A. recombination as a means of suppressing the GAL epitope.
Sequence 1340 BP; 285 A; 362 C; 391 G; 302 T; development of a DNA construct (pNeo-alpha-GT10.8B) used to The neomycin-resistance cassette given in 093078 was used in the WPI; 95-275446/36. 27-JAN-1995; IB0088 03-AUG-1995. м09520661-A1. 17-SEP-1991 (first entry) interrupt the mouse alpha-1,3-GalT gene by means of homologous (SVIN-) ST VINCENT'S HOSPITAL MELBOURNE (BRES-) BRESATEC LTD. function= linker sequences function= FLP '*tag= function= herpes simplex virus tyrosine-kinase olyA_signal product= /*tag= e /function= herpes simplex virus tyrosine-kinase /*tag= d 34 48 gaagttcctattctctagaaagtataggaacttc 81 gaagttcctatacNNNNNNNngaataggaacttc l standard; neomycin-phosphotransferase GB-027722. WO-G01911. Conservative Dapice AJF, recombinase DNA; 1311..1340 1250..1310 1189..1249 385..1188 84.6%; 7859 ₽₽ Pearse MJ, Rathjen PD; target Pred. No. 1.28e-03; Score 22; 0; Mismatches site DB 15; LTD. 10; Length 1340; Indels 0 Gaps 0

> May 14 13:50 FLP.rng

> > 5

િક 문 Matches Query Match 84.6%; Best Local Similarity 70.6%; Q44265 3131 gaagttcctattctctagaaagtataggaacttc 3164 vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of this fusion is under control of a galactodse regulated promoter which contains hybrid DNA from S. cerevisiae GAL 1-10 promoter and 23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587. W09313206-A. circular; ds. macrophage inflammatory protein; multimer; tumour therapy; psoriasis; hyperproliferation; yeast expression vector; SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha; pSW6 for expression of LD78 synthetic gene. 23-NOV-1993 (first entry) Q44265; Sequence See also 012153-012156, 012158-012162 and 012490. Sequence 7859 BP; 2317 A; 1656 C; 1600 occurring. are released specifically at the place where clot formation are present at the site of the target thrombus so the active agents can be cleaved, releasing the individual proteins which have antigene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide pression vectors in which the hirudin gene is linked to a second in E. coli K12 HW87. mid was used for the expression of a synthetic hirudin HV-1 gene gene can be excised by digestion with HindIII and BamHI. The plas-(selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli ColE1-based replicon pAT153. The visiae and contains origins of replication for both, the leu2 gene deposited in S. cerevisiae strain BJ2168 as NCIMB 40326. prophylaxis. Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and WPI; 91-208151/28 Craig S, (BRBI-) BRITISH BIO-TECHNOLOGY LTD. 08-JUL-1993. /*tag= a
/note= "base illegible in the specification" misc_difference Saccharomyces cerevisiae thrombotic activity. the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF shuttle vector capable of replcation in both E. coli and The vector is based on the 2u circle from S. cerevisiae. Disclosure; Page 71; 115pp; English. Dawson KM, link contains a cleavage site for e.g. factor X or thrombin which 34 gaagttcctatacNNNNNNNngaataggaacttc 1 i S standard; DNA; 7859 BRIT BIO-TECHN LTD. Czaplewski LG, Hunter MG, Conservative 1773 Location/Qualifiers The enzymes which cleave the fusion protein Czapleswski The plasmid can be used to construct ex-Edwards Pred. Score 22; , • Mismatches ₽, No. 1.28e-03; 5 DB Gilbert RJ; 2; 10; Indels 1600 Length 7859; <u>د</u>: 2286 T; S. cere-It is a ç. Gaps 0

May 14 13.50 FLP mg 11

THE SULTY OF ç 밁 Query Match 84.6%; Best Local Similarity 70.6%; Matches Q25185; LT 13 Q25185 3131 gaagttcctattctctagaaagtataggaacttc 3164 Protein with stem cell inhibition activity, e.g. LD78 or M1P-1 alpha - unable to form stable multimer higher than dodecamer, expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BamHI site. myocardial infarction, stroke, pulmonary embolism and deep vein 23-0CT-1991; G01860. 24-0CT-1990; GB-023149. WPI; 93-227322/28. gene in pSW6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of epidermal growth factor (EGF). The expression of this fusion is under this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha- factor pre-pro peptide fused in-frame to amipicillin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced ability for passage through E.coli and also contains the leu2 gene (a yeast selectable marker) and the coli as it contains the origin of replication for both organisms. It vector capable of replication in both S. cerevisae and on the 2 micron circle from Saccharomyces cerevisae. The sequence given is the yeast expression vector pSW6. Disclosure; Page 67; 101pp; English. sequence -New proteins comprising active protein and integrin-affinity Dawson KM, Edwards RM, Fallon A; Saccharomyces cerevisae phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss. ampicilin resistant locus; epidermal growth factor; GAL 1-10; Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; pSW6 expression vector. Sequence cerevisiae. vector pSW6 (NCIMB 40326) is based on the 2 micron circle from used to direct export of the LD78 protein. The secretion signals from the yeast mating type factor alpha were Secretion aids purification and rapid analysis of the extracellular medium after expression in S. cerevisiae. An expression vector was designed to enable secretion of LD78 to Disclosure; Page 159-168; 294pp; English. providing better tissue penetration terminated in this vector by the natural yeast PGK terminator. cerevisae phosphoglycerate kinase (PGK) promoter. hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. WPI; 92-183627/22. WO9207874-A. the alpha-factor pro-peptide. Genes to be inserted into the pSW6 the control of an efficient galactose regulated promoter which contains thrombosis (BRBI-) BRITISH BIO-TECHNOLOGY LTD 14-MAY-1992. 18-NOV-1992 34 gaagttcctatacNNNNNNNgaataggaacttc 1 standard; are antithrombotics useful in treating and preventing 7859 BP; (first entry) Conservative DNA; 2317 A; ₽₽ Pred. No. 1.28e-03; Score 22; 0 Mismatches 1698 1667 C; DB ç --The yeast expression 10; 1585 1635 G; Length 7859; **G**; Indels LD78. Transcription It is a shuttle Escherichia It is based 0. Gaps The EGF <u>.</u>

RSEBBSU

Partial FRT site lacking additional 5 FLP binding sites. Maize; Zea mays; cereal; grass; protoplast; FLP; ss.

Synthetic.

H09417176-A

Q67141;

22-MAR-1995 (first entry)

Q67141 standard; DNA; 41

ВP

May 14 13:50 FLP mg

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င္ မှ 밁 ₽ Query Match Best Local Similarity Matches Best Local Similarity Query Match Matches Q29100 3131 gaagttcctaftctctagaaagtataggaacttc 3164 the FRT has only 12 base pairs on the 3' end of the spacer. apparently missing base would be C.
Sequence 33 BP; 11 A; 5 C; 6 G; 11 T; FLP-mediated gene modification in mammalian cells - givir precise modification by recombination and can be used to (SALK) SALK INST BIOLOGICAL STUDIES Ogorman SV, Wahl GM; 08-MAR-1991; US-666252 06-MAR-1992; U01899 gene inactivation; ss. Sequence of FLP recombination target site FLP recombinase; site-specific integration system; gene activation; Q29100; are separated by 8 nucleotides. NB, in the claims the sequence combination of nucleotides so long as the two 13 base-pair repeats nucleotides in the spacer region can be replaced with any other FLP recombinase is pref. Q29101. The FLP recombination target site number of the 2-mu plasmid of S. cerevisiae during DNA replication. recombination reaction that is involved in amplifying the copy FLP recombinase is a protein which catalyses a site-specific Claim 33; Page 40; 49pp; English. transgenes for therapeutic purposes and analysis of development WPI; 92-331739/40. W09215694-A. /*tag= a /label= spacer misc feature Synthetic. 25-FEB-1992 (FRT) has been identified as minimally comprising two 13 base-pair 17-SEP-1992. The inventors claim a mammalian recombination system in which the 34 gaagttcctatacNNNNNNNngaataggaacttc 1 ų 1 gaagtteetattetetagaaagtataggaaett 33 gaagttcctatacNNNNNNNngaataggaactt standard; 23; 24; separated by an 8 base-pair spacer (see Q29100). The Conservative Conservative (first entry) 14..21 DNA; Location/Qualifiers 80.8%; 69.7%; 84.6%; 70.6%; 33 ВР Score 21; DB 5; L Pred. No. 4.88e-03; Pred. Score ç <u>.</u>. Mismatches Mismatches No. 1.28e-03 DB 4; 10; Indels 10; Length 7984; Length 33; Indels alter <u>.</u> ç Gaps Gaps **;** 0

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ESSULT

ID 005

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AC 05 RESULT
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AC N8
DT 08
DE Ba Ş 닭 S 밁 Matches Best Local Query Match Best Local Similarity Query Match N81164 standard; | N81164; JLT 16 Q51746 standard; (Q51746; 08-NOV-1990 (first entry) Base substituted E.coli beta-galactosidase alpha-fragment. cross reacted to a few non-mycobacterial spp. The probe mabe useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T; DNA conscience --Disclosure; Page 51 79pp; English.

This sequence is of the partial FRT site which is ligated into the This sequence is of the partial FRT site which is ligated into the sequence is of the partial FRT site which in the Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; additional 5 FLP protein binding sites, and has application in the construction of transgenic eukaryotic cells.

Sequence 41 BP; 13 A; 7 C; 8 G; 13 T; 27-JAN-1994; U00927. 29-JAN-1993; US-010997. Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Claim 3; Page 14; 23pp; English. WPI; 93-378844/48. Shank DD, 26-MAY-1992; US-889651 24-MAY-1993; 108325 01-DEC-1993. EP-571911-A. Synthetic. 31-MAY-1994 DNA constructs - for creating transgenic eukaryotic cells WPI; 94-264090/32. Hodges TK, Lyznik LA; 04-AUG-1994. samples detection and amplification of Mycobacteria nucleic acid (PURD) PURDUE RES FOUND (Q51735). It hybridized to all spp. of mycobacteria tested, New oligo:nucleotide probes specific for Mycobacteria - used (BECT) BECTON DICKINSON CO 12 svhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhv 45 5 agttectatactttetagagaataggaaette 36 1 gaagttcctattcNNNNNNngtataggaacttc 34 ω agttcctattcNNNNNNNngtataggaacttc 34 beta galactosidase alpha-fragment; Similarity 22; 0 Spears PA; Conservative Conservative (first entry) DNA; cDNA; 91 BP 76.9%; 68.8%; 76.9%; 204 BP Pred. No. 1.83e-02; 23; Mismatches 11 Score 20; Score 20; DB 12; Pred. No. 1.83e-02; .° Mismatches DB 12; D8 base substitutions; 9; 10, Length 91; Length 41, The probe may Indels Indels 'n <u>,</u> 0; but tor Gaps Gaps 0 9

May 14 13:50 Matches Query Match 61.5%; Best Local Similarity 18.5%; Q49264 standa Q49264; 28-APR-1994 primer_bind
/*tag= b exon exon exon occurred singularly in any given mutant. See also P80575. transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen WPI; 88-279927/40. /*tag= /*tag= /*tag= /*product= ced-4 gene_product exon 459..908 Caenorhabditis briggsae. mammal; probe; Alzheimer's disease; cell death gene; PCR; polymerase chain reaction; ciona intestinalis; echinoderm; lamprey; puffer fish; hybridisation; lower organism; structural homologue; ced-4. Sequence variable 3' ends generated in this way are used as primers for possible nucleotide positions within a specified region. The it to generate a popn of DNA molecules which terminate at all single stranded template and an oligonucleotide was hybridised E.coli beta-galactosidase. The wild type sequence was obtained Disclosure; p; English. 03-APR-1987; US-034819. 30-MAR-1988; 105163. 05-MAY-1988. EP-285123-A. misc_feature Escherichia coli. /*tag= Long-distance homology; evolution; nematode; reverse transcriptase. Nucleotides are misincorporated by the Random point mutations were introduced into the alpha fragment misincorporation, completion of molecules and screening. (SUSO) SUOMEN SOKERI OY. /function=multiple cloning site /*tag= /*tag= 159 hvchnvhbnnhrnwayvrhdarrddvh 185 29 tcctatacNNNNNNNngaataggaact 3 standard; DNA; 4093 BP a ۵ ь 5; 204 BP; (first entry) Conservative ŝ 19..69 Location/Qualifiers 459..3246 986..1081 1651..1716 1383..1472 187..204 Location/Qualifiers 21 A; Score 16; DB 1; L Pred. No. 2.91e+00; 15; Mismatches 47 C; FLP mg 17 G; 11 T; Length 204; 7; Indels 108 Others elongation, <u>,</u> Gaps ς as o. ۵, 0;

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RESULT Query Match 57.7%; Best Local Similarity 21.2%; receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Kr LT 20 Q10572 standard; DNA; Q10572; Claim 3; Fig 1; 49pp; English. The sequence was derived from the DNA encoding natriuretic peptide N-PSDB; Q10324.
Natriuretic protein receptor B - for diagnosis and treatment of (GETH) GENENTECH INC. Chang M, Goeddel D, Lowe WPI; 91-036711/05. /label= N-glycos_site Modified -site 195..197 Human Natriuretic Peptide Receptor B.
NPRB; ANP; ENP; cNP; kidney failure; heart failure; protein kinase; also affinity chromatography. Antibodies with affinity for NPRB natriuretic peptide disorders, and also to isolate peptides using 22-JUN-1990; U03586. 23-JUN-1989; US-370673. /label= N-glycos_site Modified -site 600..602 Modified -site /label= N-glycos_site Modified -site 277..279 /label= N-glycos_site Modified -site 244..246 Modified -site Modified -site Modified -site 24..26 Domain Domain Protein /label= signal sequence Peptide 09-APR-1991 (first entry) kidney failure, heart failure, hyperaldosteronism, ло9100292-A /label= N-glycos_site Modified -site 349..351 /label= N-glycos_site Modified -site 161..163 /label= N-glycos site Modified -site 35..37 /note= *GC and protien kinase Domain /note= hyperaldosteronism; glaucoma; guanyl cyclase. /label= cytoplasmic domain /label= transmembrane domain /label= extracellular domain /label= mature NPBR tomo sapiens. 14, 952). 0-JAN-1991. label= N-glycos_site be prepd. "binds natriuretic peptides 1047 The protein (or variants) can be used in treatment of ₽₽; 479..1047 Location/Qualifiers 1..22 456..456 23..455 1047 87 A; Ċ. 뫉 Score 15; activity' 15 ç A, B and DB 2; 83 G; ೧ Length 1047; 51 glaucoma etc. 7

Matches

Conservative

Pred. No. 9.70e+00; 13; Mismatches 13

Indels

<u>,,</u> Gaps

0

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RESULT
ID 07
AC 07
DT 21
DE E.
KW C: 밁 ÷ 밁 မ Matches Query Match 57.7%; Best Local Similarity 61.3%; Q71367; 21-APR-1995 (first entry) E.coli/S.cerevisiae shuttle vector pMTL8100. study, diagnosis and therapy of Alzheimer's disease Claim 8; Page 49-51; 78pp; English. Kozlowski MR, Manly SP, Neve RL; WPI; 94-101215/12. /product= Beta W09405811-A. T 21 Q56791 standard; cDNA; 1971 Cassette; gene expression; promoter; recombinant protein; Q71367 standard; determine the pattern of receptor expression in biopsy tissue, or for diagnostic imaging in vivo. Transgenic animals containing the C100-R C100-R gene. or ribozyme molecules designed on the basis of the C100-R DNA precursor protein (the C100-R) and so facilitates the elucidation of the function of C100-R and its role in the development of Alzheimers Cloning and expression of beta APP-C100 receptor - facilitating P-PSDB; R50951. 31-AUG-1993; U08229. 17-MAR-1994. antagonist; antisense; ribozyme; beta amyloid precursor protein, transgenic animal; diagnosis; detection; therapy; agonist; cDNA encoding receptor for C-terminus of beta-amyloid precursor. 07-0CT-1994 (first entry) therapeutic for alzheimers disease. Sequence 1971 BP; 620 A; 44 antagonists, or to profile other agents which are potentially effects of the beta amyloid precursor protein-C100 agonists or DNA as the transgene may be engineered to determine the in vivo sequence may be utilised to block transcription and expression of the autopsies to diagnose abnormalities of C100-R expression. disease. The cDNA encodes a receptor for the C-terminus of the beta amyloid (MCLE-) MCLEAN HOSPITAL CORP. (BRIM) BRISTOL-MYERS SQUIBB CO. 30-AUG-1993; US-938184. 31-AUG-1992; US-938184. Rattus rattus. C100~R; ss. Receptor; precursor protein; alzheimers disease; antibodies; Q56791; 31 జ 83 gttcctatacNNNNNNNngaataggaacttc 1 gaagttcctatacNNNNNNNngaataggaactt 2 savdnknyhdndnnngngcvynaasvarnashw 115 :: :: ىو 19; It may be used in hybridisation assays of biopsies or Conservative Antibodies specific for the C100-R may be used to amyloid precursor protein receptor. DNA; Location/Qualifiers 3249 ₽ Pred. No. 9.70e+00; = ::: ВP Score 15; <u>,,</u> Mismatches 440 C; DB 10; 436 G; 12; Length 1971; Indels 475 T; <u>,</u> Antisense Gaps <u>.</u>

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RESULT
ID Q7
AC Q7
D7 21
DE E.
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KW Ca
KW 5
Sy
SY
FH KW 7
FT 12
FT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         origin of replication and STB locus of the 2mu plasmid, from plasmid pWT100-U and inserting it into the unique EcoRV site of pMTLCJ. Plasmid pMTLCJ was constructed essentially by cloning a 0.8 kb BamHI fragment encoding chloramphenicol acetyltransferase (cat) from plasmid pCM4 (Close and Rodriguez, 1982) into the BamHI site of M13mp8. Single stranded DNA prepared from the resulting recombinant
                                                                                                                                                                                                                                                                                                                           Q71366 standard; DNA; 3400 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encompassing the replication region of plasmid pMTL4 (Chambers et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This shuttle vector has the replicative functions of plasmid as well as those of a S.cerevisiae plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= Chloramphenicol acetyltransferase
W09419472-A.
                                                    misc_signal
                                                                                                                      Synthetic.
                                                                                                                                              2 mu plasmid;
                                                                                                                                                                                                        Cassette; gene expression; promoter; recombinant protein;
                                                                                                                                                                                                                                      E.coli/S.cerevisiae shuttle vector pMTL8000.
                                                                                                                                                                                                                                                                    21-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                   Q71366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al., 1988),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             then blunt ended and ligated to a 1.1kb SspI/DraI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the modified cat gene excised as a 0.8 kb BamHI fragment, which was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stranded DNA of the mutated M13 recombinant was then prepared and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to eliminate restriction sites from the cat structural gene. Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was then used as a template in successive site directed mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by isolating a 1.4kb RsaI fragment which encompassed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 32-34; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein expression in bacteria and yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           esp modified yeast promoter, provides high level of recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New promoter DNA with unique SspI site at gene start position -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 94-294335/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Faulkner JDB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PUBL-) PUBLIC HEALTH LAB SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1993; GB-003988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1994; G00373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_signal
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                                                                                                                                                                             fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ataggaacttcggaataggaacttc 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= STB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= 2mu replication region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 57.7%;
Local Similarity 64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mu plasmid;
                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                 atacNNNNNNNngaataggaacttc 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3249 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to give pMTLCJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minton NP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g.
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                                                                                                                                                                             heterologous gene; clone; cloning; yeast; bacteria;
                                                            Location/Qualifiers 3154..3376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 3003..3225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        882 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 12;
Pred. No. 9.70e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone; cloning; yeast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           693 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLP,mg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 3249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The vector was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/label= 2mu

replication region

ဌ В Matches Query Match 57.7%; Best Local Similarity 64.0%; Q77789 standard; DNA; 5211 BP New promoter DNA with unique SspI site at gene start position - esp modified yeast promoter, provides high level of recombinant protein expression in bacteria and yeast Example 3; Page 30-32; 48pp; English. /codon= seq:CAA, aa:Lys w09423024-A. /*tag= eliminating the SspI restriction site using the plasmid site pVT100-U and inserting it into the unique EcoRV site of pMTLJ. Plasmid pMTLJ was derived from pMTLA (Chambers at al., 1988), by origin of replication and STB locus of the 2mu plasmid, plasmid as well as those of a S.cerevisiae plasmid. The vector was constructed by isolating a 1.4kb Rsal fragment which encompassed the misc_feature 07-APR-1994; U03441. 07-APR-1993; US-043747. misc_difference 480..482 sig_peptide Naja naja. X. laevis; Pre-pro-cobra C3 coding sequence. 077789; directed mutagenesis method. This shuttle vector has the replicative functions of an E.coli WPI; 94-294335/36. 01-SEP-1994. WO9419472-A. /*tag= c <u>G</u> misc_difference 483..485 mat_peptide /product= Pre-pro-cobra C3 G+C content; immune response; host defence; ss. Cobra; C3; third component of complement; human; mouse; rat; 26-JUN-1995 (first entry) faulkner JDB, (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD 26-FEB-1993; GB-003988. 25-FEB-1994; G00373 /product= Beta lactamase /label= STB locus /*tag= /tag= /codon= seq:GAA, aa:Asp /*tag= b 116 ataggaacttcggaataggaacttc 140 13-OCT-1994. 'tag= *tag= 25 atacNNNNNNNngaataggaacttc 1 AIND ۵ n a 16; pre-pro molecule; beta chain; alpha chain; codon usage; 3400 BP; Conservative GEORGE TOWN Minton NP; 9..74 Location/Qualifiers 9..4964 2526..2817 75..4961 444..1304 917 A; Pred. No. Score 15; 0; Mismatches 738 C; DB 12; 1 9.70e+00; 787 G; 9 Length 3400; Indels 958 T; from plasmid 9 Gaps 9

> May 14 13:50 FLP mg

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မှ 묽 Matches Query Match 57.7%; Best Local Similarity 60.6%; G+C content of cobra C3 mRNA is significantly lower at 43%. The significance of this difference is not known. C3 is thought to have chain comprises 992 amino acids and the beta chain comprises 633 residues, being 12 residues shorter than the human beta chain. Col C3 has a different codon usage compared to mammalian C3 mRNAs. The G+C content of all known mammalian C3 mRNAs is more than 53%. The 31-AUG-1992; 114838. 04-SEP-1991; IT-MI2349. Genetic; vector; integration; Kluyeromyces lactis; 255 ribosomal DNA; Saccharomyces cerevisiae; E. coli; domain; yeast; plasmid; promoter; expression cassette; HIS3; marker; transformant; human; lysozyme; HIZ; Q39050; Q39050 standard; into the mature two-chain protein by removing the signal peptide and the four Arg residues between the beta and alpha chain. The alpha molecules from human, mouse, rat and X. laevis. Cobra C3 is Claim 1; Fig 2A-2L; 155pp; English. Bredehorst event has occured. maintenance of the plasmid in E. coli and a domain which acts as an integrating unit consisting of two not contiguous sequences of the i heterologous proteins Claim 1; Fig 1; 26pp; English. Galeotti CL, Galle WPI; 93-127394/16. EP-537456-A. K.lactis/S. cerevisae genetic vector. synthesised as a pre-pro molecule that is subsequently processed The cDNA sequence of cobra C3 shows a high sequence homology with C3 This sequence encodes the cobra C3 (third component of complement). treatment of cancer DNA encoding cobra C3, P-PSDB; R63222 WPI; 94-333186/41. integrating unit consisting of two not contiguous sequences of the 2 ribosomal DNA from S. cerevisiae, flanking a genetic marker suitable integrating vector which comprises a region necessary for the stable multiple integration of DNA sequences into the genome of Kluyeromyces This sequence represents a genetic vector which allows the stable which allows stable multiple integration of DNA for prodn. of Vector for Kluyeromyces lactis and Saccharomyces cerevisiae (ISTS) SCLAVO SPA. 21-APR-1993. Synthetic. GALT; signal sequence; killer toxin; transcription termination signal; 28-JUL-1993 Sequence from K. lactis and S. cerevisiae is pref. used as a genetic marker integration plasmid, such as expression cassettes. for selection of the yeast transformants in which the integration lactis and Saccharomyces cerevisiae. This sequence can be used in an 711 aagtttctttacattgatgggaataaaaatttc 743 important functions in the immune response and host defence. Sequence 5211 BP; 1612 A; 1042 C; 1201 G; 1356 33 aagttcctatacNNNNNNNngaataggaacttc 1 2 micron plasmid; ss. 20; (first entry) Conservative Gallo E, Fritzinger DNA; 6824 Other DNA sequences may be introduced into the Riccio CVF 1 and CVF 2 - which are Š ΒP Score 15; DB 13; Pred. No. 9.70e+00; **.** Ĭ, Vogel C; Mismatches Rossolini GM, 13; Length 5211; Indels Thaller MC; used The gene HIS3 in the 1356 T; 0; Gaps 255 0,

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selection of transformants and an expression

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UP PR SOLP PR SOL NO. SOLE PR 88888888 S 맑 S 문 Best Query Match Query Match 53.8%; Best Local Similarity 18.5%; Matches LT 26 N81164 integration vector of the invention and an expression cassette comprising the K. lactis GAL7 promoter, the signal sequence of the K. lactis killer toxin, the cDNA encoding the ripe form of human lysozyme 2506 gaagttcctattccgaagttcctat 2530 production and secretion into the culture medium of human lysozym. This complete transformation vector is 7850 bp long and includes /*tag= E.coli beta galactosidase alpha-fragment; base substitutions; ss. Base substituted E.coli beta-galactosidase alpha-fragment. Sequence Sequence See also P80575. occurred singularly amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which transcriptase and the molecules are completed to forms that can be reverse transcriptase. Nucleotides are misincorporated by the possible nucleotide positions within a specified region. The it to generate a popn of DNA molecules which terminate at all single stranded template and an oligonucleotide was hybridised to E.coli beta-galactosidase. The wild type sequence was obtained Random point mutations were introduced into the alpha fragment Disclosure; p; English. misincorporation, completion of molecules and screening. Introducing random point mutations into nucleic acods by prepn of single stranded template, annealing a primer, elongation, WPI; 88-279927/40. (SUSO) SUOMEN SOKERI OY. Lehtovaara P, Knowles J, Koivula A, 03-APR-1987; US-034819. 30-MAR-1988; 105163 05-MAY-1988. EP-285123-A. primer_bind misc feature Escherichia coli. 08-NOV-1990 (first entry) N81164; plasmid from S. variable 3' ends generated in this way are used as primers for function=multiple cloning site /*tag= a (HLZ) and the transcription termination signal FLP of the 2 micron 159 hvchnvhbnnhrnwayvrhdarrddvh 185 Match 57.7%; Local Similarity 64.0%; 1 gaagttcctattcNNNNNNNngtat 25 6 tcctattcNNNNNNNnytataggaact 32 standard; DNA; 16; Š and then expressed in a suitable host-vector system. 6824 204 BP; Conservative Conservative ₽₽; cerevisiae. 19..69 187..204 Location/Qualifiers in any given mutant. 21 A; 204 BP 1815 A; 14; Pred. No. 9.70e+00; Score 15; DB 7; Pred. No. 3.13e+01, Score 14; 0 47 C; Mismatches Mismatches 1521 C; Bamford J, 17 G; DB 1; 11 T; 1726 G; Length 6824; œ 9 Length 204; Reinikainen Indels Indels human lysozyme. 108 Others; 1762 T; <u>.</u> 0; Gaps as o. Gaps the ຸດນ ç 0

ဌ В Query Match 53.8%; Best Local Similarity 42.4%; Matches N50025 N50034; N50034 Sequence encoding new modified human beta interferon polypeptides ${\tt IFNX}$ 418. N50025; (SEAR) SEARLE G D & CO. Bell LD, Boseley PG, Por WPI; 85-311944/50. New modified human beta interferon polypeptide(s) -(SEAR) SEARLE G D & CO. Bell LD, Boseley PG, Porter WPI; 85-311944/50. 04-SEP-1991 (first entry) Sequence breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mi have higher therapeutic index; improved stability against microbial New modified human beta interferon polypeptide(s) - pr plasmid transformed bacteria, with improved antiviral, Sequence encoding new modified human beta interferon polypeptides 04-SEP-1991 plasmid transformed bacteria, with P-PSDB; P50024. EP-163993-A. /*tag= Homo sapiens antiproliferative; Antiviral; cell growth regulator; Compared with interferon beta prepd. by recombinant methods, the Claim 28; Chart 21, page 43; 71pp; English. anti-proliferative and immune regulating actions P-PSDB; P50033. 17-MAY-1984; GB-012564 17-MAY-1985; 105750 EP-163993-A. Homo sapiens. antiproliterative; ss. Antiviral; cell growth regulator; 17-MAY-1984; GB-012564 17-MAY-1985; 105750. 116 aratheenatggaratgaengaraargarttye 148 for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities L1-DEC-1985. /*tag= 11-DEC-1985. FNX 485. 33 aagttcctatacNNNNNNNngaataggaacttc 1 27 standard; DNA; 501 standard; DNA; 498 a 498 BP; Conservative (first entry) Location/Qualifiers Location/Qualifiers ss. Porter 112 A; = = = = = ВP ₽₽ AG; Pred. No. 3.13e+01; AG; Score 14; 6; Mismatches 30 C; immune immune system regulator; improved antiviral DB 3; 68 G; system regulator; from incubation G; 77 T; 13; Length 498; Indels prepd. prepd. by ý <u>.</u> mixts Gaps 0

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RESULT
AC N55
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DT 04 Ş 밁 Ş В Query Match 53.8%; Best Local Similarity 22.6%; Matches Query Match 53.8%; Best Local Similarity 22.6%; Matches EP-163993-A. 11-DEC-1985. N50026; 04-SEP-1991 (first entry) N50023; Claim 28; Chart 2c, page 34; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities Sequence encoding new modified human beta interferon polypeptides 04-SEP-1991 (first entry) N50023 standard; DNA; stability. breakdown during synthesis; and better in vivo solubility and N50026 standard; DNA; 501 BP stability. breakdown during synthesis; and better in vivo solubility and Compared with interferon beta prepd. by recombinant methods, the Claim 28; Chart 2a, page 32; 71pp; English. anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) - prepd. by P-PSDB; P50022. WPI; 85-311944/50. Bell LD, Boseley PG, Porter AG; /*tag= Homo sapiens. antiproliferative; ss. Antiviral; cell growth regulator; immune system regulator; have higher therapeutic index; improved stability against microbial for cell surface receptors (allowing selective targetting); they anti-proliferative and immune regulating actions have higher therapeutic index; improved stability against 17-MAY-1984; GB-012564. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities (SEAR) SEARLE G D & CO. 17-MAY-1985; 105750 IFNX 416. 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 4 gttcctattcNNNNNNngtataggaacttc 34 4 gttcctattcNNNNNNNngtataggaacttc 34 29 မ .. --501 BP; 501 BP; They are also easier to recover from 501 BP; 107 A; 31 C; 69 G; They are also easier to recover from incubation mixts. 501 BP; 112 A; 30 C; 69 G; 85 T; Conservative Conservative Location/Qualifiers 501 BP :: :: :: Score 14; Pred. No. Pred. No. 3.13e+01 Score 14; 9; 9; 30 C; Mismatches Mismatches 3.13e+01; DB 3; DB 3; 69 G; 15; 15; Length 501; Length 85 T; incubation mixts 80 Indels Indels 501; microbial <u>.</u> <u>.</u> Gaps Gaps 0 9

S 밁 Best Loc Matches Query Match plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions Claim 28; Chart 21, page 40; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities /*tag= a EP-163993-A. (SEAR) SEARLE G D & CO. Bell LD, Boseley PG, Por WPI; 85-311944/50. 04-SEP-1991 (first entry) N50031 standard; DNA; 501 stability. breakdown during synthesis; and better in vivo solubility and anti-proliferative and immune regulating actions Claim 28; Chart 2d, page 35; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the New modified human beta interferon polypeptide(s) - puplasmid transformed bacteria, with improved antiviral, WPI; 85-311944/50. Bell LD, Boseley PG, Porter AG; 17-MAY-1984; GB-012564. 11-DEC-1985. 17-MAY-1985; 105750. Homo sapiens. antiproliferative; Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides N50031; Sequence have higher therapeutic index; improved stability against microbial P-PSDB; P50025. 17-MAY-1985; 105750. 17-MAY-1984; GB-012564. EP-163993-A. Homo sapiens. antiproliferative; Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides New modified human beta interferon polypeptide(s) -P-PSDB; P50030. (SEAR) SEARLE G D & CO. IFNX 448. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities 11-DEC-1985. IFNX 430 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 Local Similarity 4 gttcctattcNNNNNNNgtataggaacttc 501 BP; 53.8%; ilarity 22.6%; Conservative They are also easier to recover from incubation mixts. 501 BP; 108 A; 31 C; 70 G; 81 T; 1..501 Location/Qualifiers 1..501 Location/Qualifiers SS. 88. Porter 108 A; ₽₽ Score 14; DB 3; Pred. No. 3.13e+01 9; 31 C; Mismatches 34 ç 15; Length 501; Indels prepd. by 0 Gaps 0

surface receptors (allowing selective targetting); they

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KW AI Ş 맑 នននន Ş 맑 Query Match Matches Best Local Similarity Query Match Matches Query Match 53.8%; Best Local Similarity 22.6%; N50027; N50029 standard; stability. have higher therapeutic index; improved stability against mic breakdown during synthesis; and better in vivo solubility and 04-SEP-1991 T 33 N50027 standard; (SEAR) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50. Sequence encoding new modified human beta interferon polypeptides IFNX 446. antiproliferative; Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides Sequence stability. breakdown during synthesis; and better in vivo solubility and Claim 28; Chart 2g, page 38; 71pp; English. anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) -P-PSDB; P50028. EP-163993-A. antiproliferative; ss. Antiviral; cell growth regulator; immune system regulator; 04-SEP-1991 (first entry) N50029; Sequence have higher therapeutic index; improved stability against microbial 11-DEC-1985, 17-MAY-1985, 105750. Homo sapiens. IFNX 444. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities 17-MAY-1984; GB-012564. 15 bytbggnttyytbcarmgdwnnwnnaaytty 45
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:::|: ||: 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 4 gttcctattcNNNNNNNgtataggaacttc 34 4 gttcctattcNNNNNNNngtataggaacttc 34 ىھ 501 501 BP; They are also easier to recover from incubation mixts 501 BP; 112 A; 31 C; 69 G; 79 T; They are also easier to recover from 501 BP; 110 A; 30 C; 69 G; Conservative Conservative (first entry) DNA; Location/Qualifiers DNA; 53.8%; 501 BP 501 BP :: :: :: .. =:=: Score 14; DB 3; Pred. No. 3.13e+01 Score 14; DB 3; Length 501; Pred. No. 3.13e+01; 9; 9; Mismatches Mismatches 15; Length 501; 15; incubation mixts. 80 T; Indels Indels prepd. microbial ğ <u>,</u> 0 Gaps Gaps 0 0;

Ş 망 Matches Query Match 53.8%; Best Local Similarity 22.6%; /*tag= a EP-163993-A. /*tag= a EP-163993-A. anti-proliferative and immune regulating actions Claim 28; Chart 2e, page 36; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the anti-proliferative and immune regulating actions Claim 28; Chart 2j, page 41; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and New modified human beta interferon polypeptide(s) - pr plasmid transformed bacteria, with improved antiviral, breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mi Sequence 501 BP; 108 A_i 30 C_i 72 G_i 79 T_i for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial New modified human beta interferon polypeptide(s) - pr plasmid transformed bacteria, with improved antiviral, Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. antiproliferative; ss. Antiviral; cell growth regulator; Sequence encoding new modified human beta interferon polypeptides 04-SEP-1991 N50032; N50032 standard; DNA; 501 BP Sequence stability. WPI; 85-311944/50. Bell LD, Boseley PG, Porter AG; 17-MAY-1984; GB-012564. P-PSDB; P50031. 17-MAY-1984; GB-012564. 17-MAY-1985; 105750 Homo sapiens. IFNX 449. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities P-PSDB; P50026. (SEAR) SEARLE G D & CO. 17-MAY-1985; 105750 11-DEC-1985. (SEAR) SEARLE G D & CO 11-DEC-1985. 15 4 gttcctattcNNNNNNNgtataggaacttc bytbggnttyytbcarmgdwnnwnnaaytty 45 ::|: ||:|: 501 BP; They are also easier to recover from incubation mixts. Conservative (first entry) Location/Qualifiers
1..501 Location/Qualifiers
1..501 112 A; Score 14; DB 3; Pred. No. 3.13e+01 9; Mismatches 31 C; immune system regulator; μ 67 G; 15; Length 501; 80 T; Indels prepd. by prepd. 0: mixts. Gaps 9

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Query Match

Best Local Similarity

53.8%;

Pred. No. 3.13e+01; Score 14; DB 3;

Length 501;

RESULT
ID NS
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DT 045
DE See
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PD 11 Ş, B S 문 Matches Query Match 53.8%; Best Local Similarity 22.6%; Matches EP-163993-A. 11-DEC-1985. Sequence encoding new modified human beta interferon polypeptides Sequence encoding new modified human beta interferon polypeptides IFNX 417. antiproliferative; ss. Antiviral; cell growth regulator; immune system regulator; 04-SEP-1991 N50033; T 36 N50033 standard; stability. breakdown during synthesis; and better in vivo solubility and have higher therapeutic index; improved stability against microbial Claim 28; Chart 2b, page 33; 71pp; English.
Compared with interferon beta prepd. by recombinant methods, plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) -P-PSDB; P50023. Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. EP-163993-A. Homo sapiens. antiproliferative; ss. Antiviral; cell growth regulator; immune system regulator; 04-SEP-1991 (first entry) N50024 N50024 standard; DNA; 501 BP Homo sapiens. IFNX 456. anti-proliferative and immune regulating actions 17-MAY-1984; GB-012564 'tag= for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities (SEAR) SEARLE G D & CO. 17-MAY-1985; 105750. 11-DEC-1985. /*tag= 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 4 gttcctattcNNNNNNNngtataggaacttc 4 gttcctattcNNNNNNNngtataggaacttc 34 35 a 501 BP; Conservative They are also easier to recover from incubation mixts Conservative (first entry) Location/Qualifiers DNA; Location/Qualifiers 501 BP 110 A; Score 14; DB 3; L Pred. No. 3.13e+01; 9; Mismatches 9; 32 C; Mismatches ω 66 G; 15; 15; Length 501; 81 Indels Indels prepd. 7 ьy ç <u>.</u> Gaps Gaps 0 0

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밁 Ş В May 14 13:50 Query Match 53.8%; Score 14; DB 3; L Best Local Similarity 22.6%; Pred. No. 3.13e+01; Matches Query Match 53.8%; Best Local Similarity 59.4%; Matches 1327 aaatttcttttctatgaataatagaggaactt 1358 diagnosis and treatment, esp. for the treatment of cystine urine sequenced. The sequence is expected to be useful for genetic rat cDNA clone RL-39(10) as probe. One clone (I)-1 was purified, Claim 3; Fig 2; 9pp; Japanese. This sequence encodes human cysteine dioxygenase. A cDNA library was urinary diseases WPI; 92-197392/24. 01-MAY-1992. cystine; genetic diagnosis; cystine urine diseases; ss. Encodes human liver cysteine dioxygenase. Q25420 standard; DNA; 1561 BP. Q25420; have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 111 A; 31 C; 68 G; 80 T; Claim 28; Chart 2k, page 42; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities diseases, tissue from a liver cancer patient. The library was screened with prepared using polyA+ RNA separated from human non-cancer liver Human liver cysteine di:oxygenase and cDNA used for its encoding P-PSDB; R24407 (AJIN) AJINOMOTO KK. 20-SEP-1990; JP-251647. 20-SEP-1990; J04131083-A. Homo sapiens. 30-NOV-1992 (first entry) for cell surface receptors (allowing selective targetting); they anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) - prepd. by P-PSDB; P50032. WPI; 85-311944/50. Bell LD, Boseley PG, Porter AG; (SEAR) SEARLE G D & CO 17-MAY-1984; GB-012564. 17-MAY-1985; 105750 is used for diagnosis and treatment of cystine-associated 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 ~ 4 gttcctattcNNNNNNNgtataggaacttc 34 aagttcctattcNNNNNNNgtataggaactt 33 19; ; and cystine diseases. 1561 BP; 251647. Conservative Conservative Location/Qualifiers 230..830 474 A; :: = = = = Score 14; DB 4; Pred. No. 3.13e+01 0; 9; Mismatches Mismatches 342 C; FLP.mg 337 13; Length 1561; 15; Length 501; ç Indels Indels 408 <u>;</u> **;**: Gaps Gaps and 0 0

RESULT
ID Q44
AC Q4A
AC Q4A
D7 16
D7 16
D8 Hu
KW In
KW In
KW In
CI
FT /I
FT /I မှ В Matches Query Match Best Local Similarity 1171 cctctacagtgtacacaatgggaacttc 1198 Q47839; Q47839 standard; 01-SEP-1994. 25-FEB-1994; G00373. /product= Chloramphenicol acetyltransferase WO9419472-A. S 21-APR-1995 (first entry) Q71367 standard; DNA; 3249 expression of the IL-9 receptor protein and to probe for the IL-9 cytokine. produce IL-9 receptor or as probes for cells which respond to the Claim 6; Page 18; 30pp; English. The interleukin (IL) 9 receptor nucleic acid sequence can be used Nucleic acid encoding interleukin-9 receptor - used to Homo sapiens Interleukin 9 receptor; IL-9; Human interleukin 9 receptor clone ph9RA6. /label= 2mu replication region. misc feature 2375..2666 misc signal Synthetic. 2 mu plasmid; fermentation; Cassette; gene expression; promoter; recombinant protein; E.coli/S.cerevisiae shuttle vector pMTL8100. Q71367; Sequence IL-9 receptor levels. to the receptor and for qualitative and quantative measurement of the IL-9 receptor can be used therapeutically to block IL-9 binding IL-9 receptor agonists and antagonists. Antibodies directed against coding sequences. Transfected cell lines can be used to screen for reagents used in diagnosis and therapy involving interleukin WPI; 93-303390/38. Druez C, 09-MAR-1992; US-847347. 25-FEB-1993; U01720. NO9318047-A. /*tag= a /product= Interleukin 9 receptor. antagonist; ss /*tag= /label= STB locus. /*tag= /*tag= (LUDW-) LUDWIG INST CANCER RES. [6-MAR-1994 (first entry) 28 cctatacNNNNNNNngaataggaacttc 1 ი Renauld J, The complementary sequences can be used to inhibit the 1997 BP; Conservative Ġ heterologous Location/Qualifiers 3003..3225 461..1117 188..1798 Location/Qualifiers 53.8%; Van Snick J; 388 A; 1997 gene; ₽. Pred. No. Score 14; ₽₽ • antibodies; therapy; probe; agonist; Mismatches 612 C; clone; cloning; yeast; bacteria; 3.13e+01 DB 8; 593 G; 11; Indels Length 1997; 404 T; produce 0; 98 Gaps ç 0

May 14:13:50 FLP.mg

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Ş 뭉 RESULT Best Matches Query Match constructed by isolating a 1.4kb Rsal fragment which encompassed the origin of replication and STB locus of the 2mu plasmid, from plasmid pVT100-U and inserting it into the unique EcoRV site of pMTLCJ. Plasmid pWTLCJ was constructed essentially by cloning a 0.8 kb BamHI fragment encoding chloramphenicol acetyltransferase (cat) from plasmid pWM4 (Close and Rodriguez, 1982) into the BamHI site of plasmid pWM4 (Close and Rodriguez, 1982) into the BamHI site of Q71366 standard; DNA; /*tag= encompassing the replication region of plasmid pMTL4 (Chambers M13mp8. esp modified yeast promoter, provides high level of recombinant misc_feature E.coli/S.cerevisiae shuttle vector pMTL8000. Q71366; stranded DNA of the mutated M13 recombinant was then prepared and the modified cat gene excised as a $0.8\ \mathrm{kb}$ BamHI fragment, which wa to eliminate restriction sites from the cat structural gene. Double was then used as a template in successive site directed mutagenesis 26-FEB-1993; GB-003988. esp modified yeast promoter, provides high level of recombinant protein expression in bacteria and yeast New promoter DNA with unique SspI site at gene start position WPI; 94-294335/36. (PUBL-) PUBLIC HEALTH LAB Faulkner JDB, Minton NP; 26-FEB-1993; GB-003988. 25-FEB-1994; G00373 01-SEP-1994. WO9419472-A. misc_signal Synthetic. Cassette; gene expression; promoter; recombinant protein; 21-APR-1995 (first entry) Sequence al., 1988), then blunt ended and ligated to a l.lkb SspI/DraI fragment plasmid as well as those of a S.cerevisiae plasmid. This shuttle vector has the replicative functions of Example 3; Page 32-34; 48pp; English protein expression in bacteria and yeast New promoter DNA with unique SspI site at gene start position -WPI; 94-294335/36. Faulkner JDB, /product= Beta /*tag= /label= /label= 2mu replication region termentation; (PUBL-) PUBLIC HEALTH 103 ttctagctagagaataggaacttc 126 mu plasmid; 11 ttcNNNNNNngtataggaacttc 34 Match 53.8%; Local Similarity 62.5%; a STB locus 15; Single stranded DNA prepared from the resulting recombinant 3249 BP; to give pMTLCJ. Conservative ds. Minton NP; heterologous gene; clone; cloning; yeast; bacteria; lactamase. Location/Qualifiers 3154..3376 444..1304 2526..2817 LAB 3400 882 A; SERVICE BOARD. SERVICE ВP Score 14; Pred. No. 693 C; No. 3.13e+01 BOARD. DB 12; Length 3249; 743 G; Indels an 931 T; The vector was E.coli 0 Gaps et 0

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S 밁 Query Match Best Local S Matches exon exon exon exon exon hybridisation; lower organism; structural homologue; Alzheimer's disease; cell death gene; PCR; polymerase chain reaction; ciona intestinalis; echinoderm; lamprey; puffer fish; pVT100-U and inserting it into the unique EcoRV site of pMTLJ. Plasmid pMTLJ was derived from pMTL4 (Chambers at al., 1988), by This shuttle vector has the replicative functions of an E.coli plasmid as well as those of a S.cerevisiae plasmid. The vecto exon exon /*tag= exon ced-4 Q49264 standard; DNA; 4093 BP. directed mutagenesis method. eliminating the SspI restriction site using the plasmid site origin of replication and STB locus of the 2mu plasmid, from plasmid constructed by isolating a 1.4kb RsaI fragment which encompassed the Example used to identify DNA that codes for evolutionary conserved P-PSDB; R42742. WPI; 93-336943/42. 01-APR-1992; US-861458. (CAMB-) CAMBRIDGE NEUROSCIENCE INC. 01-APR-1993; U03102. W09320237-A. /*tag= /*tag= /*tag= /*tag= Caenorhabditis briggsae. Long-distance homology; evolution; nematode; 28-APR-1994 (first entry) Q49264; aminoacid sequences Long-distance homology cloning of genes from lower organisms Johnson CD, 14-0CT-1993. /*tag= /*tag= /*tag= Disclosure; Fig 8; /*tag= /*product= 103 ttctagctagagaataggaacttc 126 11 ttcNNNNNNNgtataggaacttc 34 closure; Fig 8; 188pp; English.
primers/probes (Q49266-Q49295) are used to isolate the ced-4 h 53.8%; Similarity 62.5%; ρ O Б 3; Page 15; ced-4 3400 BP; Marchionni MA; Conservative ds. Location/Qualifiers 459..3246 30-32; 48pp; English. 2477..2752 1383..1472 986..1081 _gene_product 459..908 3031..3246 2802..2906 1834..2172 651..1716 917 A; Score 14; DB 12; Pred. No. 3.13e+01 0; Mismatches 738 C; 787 ç; Length 3400; Indels 958 T; The vector was 0 Gaps 0

£ В May 14 13:50 Matches Query Match 53.8%; Best Local Similarity 58.8%; 3228 gaagttcacatcccaatagctgtataagaatttc 3261 gene from the nematode C. briggsae. /*tag= g /product= repeat_unit
/*tag= c SIVmac239 nef-deletion. Q24802; Q24802 standard; Simian immunodeficiency virus. PCR; site-directed mutagenesis; retrovirus; Macaque; monkey; polymerase chain reaction; 06-JUL-1992 (first entry) exon S S primer_bind /note= "full-length product exon 6528..6597 /product= /product= /*tag= /*tag= h /*tag= /*tag= repeat_unit /rpt_type= OTHER /note= "U3" repeat_unit /note= "i.e. 5' repeat_region /*tag= l /product= tat /*tag= k /*tag= /product= vif /product= standard_name= /note= "U5" 'rpt_type= OTHER /*tag= /note= "R" rpt_type= /*tag= 'rpt_type= TERMINAL /*tag= 34 gaagttcctatacNNNNNNNngaataggaacttc 1 σ 20; 설 Ą ጀ gag Conservative 1..818 LTR* tRNA_PBS 1053..2585 518..600 5340..5984 822..849 601..818 DNA; 6302..6597 6051..6456 5812..6150 2228..5410 Location/Qualifiers 10097 ВP obtained by Score 14; DB 9; I Pred. No. 3.13e+01; 0; Mismatches 14; FLP mg splicing. null mutation; 726 Length 4093; ç Indels 1346 SS 0 7 Gaps <u>.</u>.

/note= "full-length product obtained by splicing"
CDS 6604..9243

/product= rev

May 14 13:50 HIP mg ယ္သ

/*tag=

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deletion was confirmed by DNA sequencing. The fragment contq. the deletion was cloned into p239SpE3' to yield p239S-E3' (nef-deletion) which was digested with SphI and ligated to SphI-cut p239SpSp5'. claim 1; Fig 1; 51pp; English.

Parental virus SIVmac239 was isolated from a macaque monkey (see 022487). An SstI fragment of p239SpE3' contg. the C-terminus of the nef gene was cloned into M13 and subjected to site-directed mutagenesis. A 73mer primer was used which was complementary to bases 9215 through 9250 and 9433 through 9469. Since bases 9251 /*tag= exon exon Primate lentivirus vaccine protecting against AIDS - and primate lentiviruses and their DNA clones contg. null mutations, useful for /*tag= GC_signal /*tag= The ligation product was used to directly transfect cultured cells. See also 021075-8. not included in the newly synthesised negative strand. Successful through 9432 were not included in the primer, their complement was producing vaccine P-PSDB; R22365-R22371, R24126-7. Desrosiers RC. WPI; 92-056816/07. ₩O9200987-A. polyA_signal TATA_signal GC_signal GC_signal GC_signal misc_signal /rpt_type= TERMINAL
/note= "i.e. 3' LTR /product= 10-JUL-1991; U04884. 12-JUL-1990; US-551945. /standard /standard /*tag= /standard /standard /standard repeat_region /product= nei /product= rev /note= "see /product= (HARD) HARVARD COLLEGE 23-JAN-1992. /*tag= /*tag= /*tag= 'note= "see /*tag= o /*tag= ש = _name= tat env name= name= name≃ _name= 10097 above" above* LTR" 415..424 NF Kappa 429..438 Spl_binding_site 462..471 Spl_binding_site 451..460 Spl_binding_site 440..449 Spl_binding_site 488..494 9280..10097 8803.,9059 8803..8902 ₽P; 9950..9955 9077..9686 3387 A; 1911 C; 2527 G;

Query Match 53.8%; Score 14; DB 3; L Best Local Similarity 61.5%; Pred. No. 3.13e+01; Length 10097;

/product= tat

May 14 13:50 Matches 16; Conservative 0; Mismatches FLP.mg 10*;* Indels 0 Gaps 0

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agttcctctactgtaaaatgaattgg

7821

primer_bind
/*tag=_e /product= repeat_unit /*tag=_d repeat_unit
/*tag=_ b T 43 Q22487 standard; DNA; 10279 BP exon exon 06-JUL-1992 exon /*tag= Macaque; monkey; mac239; polymerase chain reaction; PCR; site-directed mutagenesis; retrovirus; ss. SIVmac239 proviral genome. Q22487; /product= /rpt_type= OTHER /note= "U5" /rpt_type= OTHER /note= "U3" /rpt_type= TERMINAL
/note= "i.e. 5' LTR repeat_region /*tag=_a Simian immunodeficiency virus /product= /*tag= /product= rev /*tag= /note= "full-length product obtained by splicing" /product= tat /*tag= /*tag= /product= /*tag= /product= /*tag= g /product= gag /*tag= f standard_name= /note= "R" rpt_type= OTHER repeat_unit tag= note= *tag= 32 agttcctatacNNNNNNNngaatagg *full-length product obtained by splicing* 6604..9243 = * 5 B env ŽÍ. g 전 Ğ (first entry) 1..818 1053..2585 LTR. 601. 1..517 518..600 822..849 8803..8902 6528..6597 6302..6597 5812..6150 5340..5984 6051..6456 2228..5410 Location/Qualifiers

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above"

8803..9059

note= see /product= rev /*tag= /note= "see

above"

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Matches

Best Local Similarity 61.5%;

Pred. No. 3.13e+01;

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36

Conservative

0;

Mismatches

10;

Indels

0; Gaps

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7796 agttcctctactgtaaaatgaattgg 7821

32 agttcctatacNNNNNNNngaatagg 7

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polyA_signal
/*tag= x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GC_signal
/*tag= v
                                                                                                                                                         from 10-20kb EcoRI fragments (EcoRI is a non-cutter of SIVmac239). The library was screened with pK2 BamA as probe and a full-length molecular clone was isolated and sequenced. Then, EMBL-SIVmac239
                                                                                                                                                                                                   supernatant. Total cell DNA was prepared from SIVmac239-infected cells and digested with EcoRI. An EMBB-4 library was constructed
                                                                                                                                                                                                                                characteristic of SIV infection were co-cultivated with HuT-78 cells. Infectious SIVmac239 virus was identified in the cell
                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                      Primate lentivirus vaccine protecting against AIDS - and primate lentiviruses and their DNA clones contg. null mutations, useful i
                                                                                                                                                                                                                                                                                                                                                     WPI; 92-056816/07
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nef-deletion mutant. See also Q21075-8.
Sequence 10279 BP; 3465 A; 1936 C;
                                            generate the full-length genomic sequence and to produce the
                                                                                     SphI. A 6361bp fragment from viral nucleotide 6452 to the EcoRI
                                                                                                                6451, was inserted in vector pBS(+) to produce subclone p239SpSp5'
                                                                                                                                                                                                                                                              Cell-free serum samples from a macaque monkey exhibiting symptoms
                                                                                                                                                                                                                                                                                           producing vaccine
                                                                                                                                                                                                                                                                                                                                   P-PSDB; R22365-R22372, R24126.
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/note= "i.e. 3' LTR'
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                             preferred null-mutations of the invention. See Q24802
                                                         pBS(-) to produce subclone p239SpE3'. These subclones were used to
                                                                     site in the right flanking cellular sequence, was inserted in
                                                                                                    In a separate reaction, EMBL-SIVmac239 was digested with EcoRI
                                                                                                                               in the left flanking cellular DNA sequence to viral nucleotide no.
                                                                                                                                             was digested with SphI and a 6706bp fragment, contg. the SphI site
                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1991; U04884.
12-JUL-1990; US-551945.
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429..438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10132..10137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9462..10279
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 2569 G;
                              for
                                                                                                                                                                                                                                                                                                          useful for
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Query Match

53.8%;

Score 14;

DB ۳

Length 10279;

___y= p mat_peptide /*tag= α ma* /*tag= o
mat_peptide
/** /*tag= a misc_binding /*tag= q mat_peptide mat_peptide
/*tag= h intron /*tag= exon exon 054676; exon /*tag= T 44 Q54676 standard; DNA; 12151 /*tag= intron /*tag= mat_peptide /*tag= mat_peptide mat_peptide mat_peptide mat_peptide /*tag= mat_peptide /*tag= mat_peptide transit_peptide transit_peptide TATA_signal Oryza sativa reverse transcriptase; plaques; ds. Rice; starch; transit peptide; Rice starch 03-AUG-1994 /*tag= /*tag= mat_peptide /*tag= /*tag= /*tag= /*tag= /*tag= transit_peptide CAAT_signal /*tag= promoter /*tag= '*tag= *tag= n Ħ ь Ø Ω ۷ = branching enzyme gene. (first entry) 5821..5853 9862. 9595. 9019. 8519. 5854..6028 3546..3608 3360..3443 636..335 5821..6028 3609..5820 3546..3608 3444..3545 8245..8361 6648..6917 6144..6231 3291..3296 3221..3225 3164..3172 Location/Qualifiers 3352..3443 10409..10609 10210..10326 10011..1009 1026..7932 .9929 .9126 .8581 ВP pectin; cereal; aminopectin; seeds;

cereal particles by introducing the basic sequence into a rice plant. This process can be used to improve the taste of the rice. Sequence 12151 BP; 3273 A; 2479 C; 2506 G; 3890 T;

The sequence shows a gene encoding a branching enzyme of rice starch. The enzyme can be used to modify aminopectin content of starch in

Claim 4; Page 10-11;

21pp; Japanese.

\$ B

9848 aagtteetttteaggttattgtetttgaac 9877

2 aagttcctattcNNNNNNNgtataggaac 31

Matches

18;

Conservative

Query Match 53.8%; Best Local Similarity 60.0%;

Score 14; DB 10; Length 12151; Pred. No. 3.13e+01; 0; Mismatches 12; Indels 0

0; Gaps

0;

May 14 13:50

FIP mg

FLP.mg

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38
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/*tag= au
polyA_signal
/*tag= av
                              03-DEC-1993.
30-MAR-1992; 102499.
20-SEP-1991; JP-268617.
(MITS-) MITSUI GYOSAI SHOKUBUTU BIO KENKYUSHO
WPI; 94-011022/02.
                                                                /*tag= ax
J05317057-A.
                                                                                    polyA_signal
/*tag= aw
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3'UTR
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    Gene CDNA for rice starch branching enzyme for varied amino pectin in cereal - comprises structural gene specified by bas sequence introduced in rice plant for improved taste, for DNA
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RESULT
ID Q6
AC Q6
ULT 45
Q62137 standard; Q62137;
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TATA_signal
                                                                                                                                                                                                                                                                                                                  Rice starch branching enzyme gene.
Rice starch branching enzyme; oryza sativa; amylopectin; albumen;
                                                   exon
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exon
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                                                                                                                                                                                                                                                                                                             starch; ss.
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      /*tag= l
/label= Intron
                                          /*tag=
                                                                 /*tag=
                                                                                protein."
                                                                                      bases 5854-6028 encode a region of the mature
                                                                                                                                                                                /label= Intron
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                     intron
                             /note=
                                   /label=
                                                          /label= Intron
                                                                         intron
                                                                                               /note= "Bases 5821-5853 encode the transit peptide
                                                                                                      /label= Exon 3.
                                                                                                              /*tag=
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5821..6028
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       4.
                     protein coding region. 6214..6647
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3609..5820
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3444..3545
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6648..6917
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May 14 13:50 FI.P.mg

39

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FI.P.mg

8

/*tag=

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exon exon exon exon /*tag= /label= exon intron /label= exon /*tag= exon /*tag= exon /*tag= p /label= Intron /label= Intron 12. /note= "Mature protein coding region." intron 10092..10209 /label= Intron 11 intron exon intron note= /label= /label= note= /label= Intron /note= "Mature protein coding region." intron 9697..9861 /label= Exon 10 /label= Intron /*tag= /*tag= /label= Intron /note= "Mature protein coding region."
intron 8582..9018 /label= Intron intron intron /note= /label= Exon /label= Intron /*tag= /note= "Mature protein coding region."
intron 6918..7025 /*tag= m /label= Exon 5. note= "Mature 'label= 'label= Exon 8. note= "Mature 'label= Exon "Mature protein coding region." 10327..10408 *Mature protein coding region.*
9930..10010 "Mature Intron 13. = Exon 13. Exon 12. Exon 11. Exon 9. л 9. 9595..9696 л 8. 9019..9126 л 7. 8519..8581 л 6. 8245..8361 л 5. 7026..7932 110. 9862..9929 protein coding region. 9127..9594 protein coding region. 8362..8518 protein coding region. 7933..8244 10409..10865 10210..10326 10011..10091

ae

Ş 밁 Query Match Best Local S Matches polyA_signal 10865..1 /*tag= ai J0609865-A. 12-APR-1994. 30-MAR-1992; JP-102500. 30-MAR-1992; JP-102500. polyA_signal
/*tag= ah 9848 aagtteetttteaggttattgtetttgaac 9877 increasing the content of amylopectin in albumen starch and thus enabling efficient mass production of various proteins. Sequence 12151 BP; 3269 A; 2470 C; 2518 G; 3891 T; polyA_signal /*tag= ag The introduction of the rice starch branch-forming enzyme gene into a rice increase the activity of this enzyme in the plant, thereby 3'UTR used to increase the amylopectin content of albumen Claim 1; Page 16-21; 24pp; Japanese (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO. WPI; 94-155835/19. /note= "Bases 10409-10609 encode a region of mature protein. Bases 10610-10612 are the Transgenic rice containing the rice starch branch family enzyme translation termination signal, i.e. a stop /*tag= 'label= Exon 14 aagttcctattcNNNNNNNgtataggaac 31 ch 53.8%; il Similarity 60.0%; 18; Conservative af 10610..10865 0865..10888 .0839..10842 .0814..10817 Score 14; DB 12; Length 12151; Pred. No. 3.13e+01; <u>,,</u> Mismatches the 12; Indels <u>,</u> Gaps 0

Job time : 56 secs. Search completed: Tue May 14 13:59:39 1996

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue May 14 13:59:57 1996; MasPar time 25.23 Seconds 484.494 Million cell updates/sec

Tabular output not generated.

N.A. Sequence: Perfect Score: Description: Title: Comp: (1-34) from frt.seq 26 Ą.i.

1 gaagttcctattcNNNNNNNgtataggaacttc 34 cttcaaggataagNNNNNNNNcatatccttgaag

Scoring table: TABLE default Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST29 30:EST30 33:EST33 32:EST33 33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38 39:EST39 40:EST40 41:EST41 42:EST42 42:EST43 44:EST44 45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST56 51:EST51 52:EST55 53:EST53 54:EST54 55:EST55 56:EST56 57:EST57 58:EST55 59:EST59 60:EST60 61:EST61 62:EST68 69:EST69 70:EST70 71:EST77 72:EST72 73:EST73 74:EST74 75:EST75 76:EST76 77:EST73 78:EST78 79:EST79 80:EST80 81:EST81 82:EST88 84:EST88 84:EST88 85:EST89 86:EST86 93:STS5 94:STS6 87:EST87 88:EST88 89:STS1 90:STS2 91:STS3 92:STS4 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 :EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

EST-STS-TWO

Database:

95:qnEST1 96:qnEST2 97:qnEST3 98:qnEST4 99:qnEST5 100:qnEST6 101:qnEST7 102:qnEST8 103:qnEST9 104:qnEST10 105:qnEST11 106:qnEST1 107:qnEST1 108:qnEST3 109:enEST1 110:enEST3 112:enEST4 113:enEST5 114:enEST6 115:enEST7 116:enEST8 117:enEST9 118:enEST10 119:enEST11 120:enEST12 121:enEST13 122:enEST14 123:enEST15 .24:enEST16 125:enEST17 126:enEST18 127:enEST19

> May 14 13:59 128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 6.755; Variance 1.297; scale 5.207

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALI GNMENTS

LOCUS	RESULT
RICS2602A	_
308 bp	
ERNA	
EST	
11-NOV-1994	

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SOURCE KEYWORDS ACCESSION DEFINITION

to mRNA.

Oryza sativa (strain Nipponbare) Etiolated shoot (8 days old)

D40544 Rice cDNA,

partial

sequence (S2602_1A)

EST (expressed sequence tag).

May 14 13:59

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JOURNAL Unpublished (1995) The WashU-Merck EST Project Waterston, R., Williamson, A., Wohldmann, P. and

COMMENT

Washington University School of Medicine WashU-Merck EST Project 4444 Forest Park Parkway, Box 8501, St. Contact: Wilson RK GDB: G00-403-625 Email: est@watson.wustl.edu 314 286 1800 314 286 1810 Louis, MO

High quality sequence stops: 37 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information.

FEATURES source NCBI gi: 776335 /clone="31278" /organism="Homo sapiens" ocation/Qualifiers

ORIGIN BASE COUNT 99 ø /note="human" 126 c 93 p 119 t 1 others

Length 438;

Gaps

0

Query Match

S В Best Local Similarity Matches 32 ttcctattccctgcaatgtatagg 55 5 ttcctattcNNNNNNNgtatagg 28 Conservative 61.5%; Score 16; DB 39; Pred. No. 9.06e-04 0 Mismatches œ Indels <u>.</u>.

DEFINITION SOURCE KEYWORDS ACCESSION POCOR RESULT w ym19h09.r1 H14983 EST. H14983 Bonaldo. normalization. Library constructed by Bento Soares and M.Fatima 462 bp mRNA EST Homo sapiens cDNA clone 48660 5' 27-JUN-1995

REFERENCE AUTHORS ORGANISM JOURNAL Homo sapiens Unpublished (1995) Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; The WashU-Merck EST Project Wilson, R. Hillier, L., Clark, N., Dubuque, T., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; (bases 1 to 462) Elliston, K., Hawkins, M., Marra, M.,

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RESULT
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Best Local Similarity 66.7%;
                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                               Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 463)

1 (bases 1 to 463)

1 (bases 1 to 463)

1 (bases 1 to 463)
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                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAC-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
Source: IMAGE Consortium, LLNL
                  High quality sequence stops: 252
                                            Email: est@watson.wustl.edu
                                                                   Fax: 314 286 1810
                                                                                          Tel: 314 286 1800
                                                                                                                                  Washington University School of Medicine
                                                                                                                                                           WashU-Merck EST Project
                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-CTCGAGTTTTTTTTTTTTTTTT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human clone=117434 library=Stratagene lung (#937210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDB: G00-421-201
                                                                                                                                                                                                                                                                                                                                                                                                            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
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Pred. No. 9.06e-04;
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RESULT
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Best Local Similarity 63.3%;
                                             Matches
                                                          Best Local
                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI gi: 718335
                                                                                                                                                                                                                               NCBI gi: 428353
                                                                                                                                                                                                                                                                                      Phone: 0298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (2-NOV-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Commelinidae; Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST(expressed sequence tag).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICR2068A
                                                         57.7%;
Similarity 60.6%;
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                                                                                                                                                                                                                                                                                                    Japan
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                                                                                                                                                                                                                                                                                                                               Kannondai 2-1-2
                                                                                                                                                                                                                                                                                                                                              National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                              Dept. Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                           Yuzo Minobe
                                                                                                                                                                                                                                                                                                                                                                                                                     Rice cDNA from root
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the
                                             20;
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                                                                                                                                             /sequenced_mol="cDNA to mRNA"
                                                                                                                                                            /dev_stage="Seedling"
                                                                                                                                                                          /strain="Nipponbare"
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                                                          Score 15;
Pred. No.
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RESULT 7 LOCUS DEFINITION ACCESSION KEYWORDS	рь 49 q Qy 1 q	Query Match Best Local Matches	FEATURES source BASE COUNT ORIGIN		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ORGANISM	RESULT 6 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE
R07677 288 bp mRNA EST 05-APR-1995 ye98d03.rl Homo sapiens cDNA clone 125765 5'. EST.	gaagttoctattacttottatgattgggagott 81 	ch 57.7%; Score 15; DB 35; Length 288; 1 Similarity 60.6%; Pred. No. 1.91e-02; 20; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	NCBI gi: 759600 Location/Qualifiers 1288 /organism="Homo sapiens" /clone="125765" /note="human" 90 a 49 c 45 g 104 t	Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu High qality sequence stops: 248 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	Trevaskis, E., Waterston, K., Williamson, A., Wonlomann, F. and Wilson, R. The WashU-Merck EST Project Unpublished (1995) Costact: Gilcon by	rrhini; Hominidae; Homo. buque,T., Elliston,K., Hawkins,M., buque,T., Le,M., Lennon,G., Marra, ucaba,T., Le,M., Tan,F., bullismon harran bar	d CDNA was primed with a Pac I - oligo(dT) primer (5' GAAGAATTAATTAAATAACATCTTTTTTTTTTTTTTTTT	R07677 288 bp mRNA EST 05-APR-1995 ye98d03.rl Homo sapiens cDNA clone 125765 5'. R07677 EST. buman clone=125765 library=Soares fetal liver spieen lNFLS hector=pT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st

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ORGANISM Homo sapiens Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 288)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Parvaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,I Wilson,R. The WashU-Merck EST Project

TITLE The WashU-Merck EST Project JOURNAL Unpublished (1995)

COMMENT UND

Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High qality sequence stops: 248
High qality sequence stops: 248
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 759600
Location/Qualifiers
source 1..288
/organism="Homo sapiens"
/clone="125765"
/note="human"

BASE COUNT

9

49 c

45 g

104 t

Query Match 57.7%; Score 15; DB 35; Length 288; Best Local Similarity 60.6%; Pred. No. 1.91e-02; Matches 20; Conservative 0; Mismatches 13; Indels 0; Gaps

0

RESULT RE BASE COUNT FEATURES REFERENCE ORGANISM Query Match 57.7%; Best Local Similarity 64.3%; Matches JOURNAL AUTHORS 09-JAN-1995 (Rel. 42, 08-SEP-1995 (Rel. 45, Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Bult C.J., Lee N., Adams M.D., Homo sapiens pregnancy-specific (HT:2583). EST79508 Homo sapiens cDNA similar to beta-1-glycoprotein HS41410 source 1 - 381T29414; 224 gaagatccnatacagngataaaaatagg 251 34 gaagttcctatacNNNNNNNngaatagg 7 Homo sapiens NCBI Washington University School of Medicine Unpublished Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Bonaldo. normalization. Library constructed by Bento Soares and M.Fatima digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of High quality sequence stops: 58 4444 Forest Park Parkway, Box 8501, St. Louis, WashU-Merck EST Project Contact: Wilson RK The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, Fax: 314 286 1810 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and IMAGE Consortium (info@image.llnl.gov) for further information. ⊒mail: est@watson.wustl.edu 18; (bases 1 to 353) standard; RNA; EST; 381 BP Kerlavage A.R., Fleischmann R.D., Fulc Lee N., Kirkness E.F., Weinstock K.G., gi: 917270 91 314 286 1800 Conservative (human) ۵ı /note="human" /clone="192238" Location/Qualifiers /organism="Homo sapiens" (1995)68 C Last updated, Version 2) Created) Score 15; DB 16; Pred. No. 1.91e-02; <u>.</u>. 74 g Mismatches TIMI 106 t 10; Fuldner R.A., Length 353; 14 others Indels Gocayne J.D., Mammalia; Hominidae. MO 63108 ç Gaps ç

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SOURCE FTT မ 밁 TOCUS REFERENCE KEYWORDS ACCESSION DEFINITION AUTHORS ORGANISM Matches Query Match Query Match 57.7%; Best Local Similarity 64.0%; Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; ILRINA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Sequence 611512 Other_ESTs: THC24005 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Coleman T.A., Weidman J.F., Li Y., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., source additional sequence and expression information related to this EST, Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, Unpublished. Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T., Glodek A., Gnehm C.L., FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 313 gaagctcctatactacatgtggaat 337 34 10 gaagttcctatacNNNNNNNngaat 10 Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Homo sapiens EST pregnancy-specific (HT:2583).
T29414 EST79508 Homo sapiens cDNA similar to beta-1-glycoprotein 1 (bases 1 to 381) human primer=M13-21 library=Human Placenta. Saudek,D.M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; 16; 381 BP; 107 A; Conservative Collins E.J., Dimke D., Feng P., Ferrie A., <1..>381 /organism="Homo sapiens" /note="human" Location/Qualifiers Shirley, R., Blake J.A., 381 bp Hanna M.C., Hedblom E., Hinkle Jr P.S., 78 C; 71 G; 125 T; 0 other; Score 15; DB 119; Pred. No. 1.91e-02; 0; Mismatches Small, K.V., Brandon R.C., DB 119; Length 381; Spriggs, T.A., Utterback, T.R., 9; Indels Chiu M.W., Geoghagen N.S.M., Fuldner, R.A., 06-SEP-1995 0; Gaps <u>.</u>

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COMMENT KEYWORDS ACCESSION Pocus ORIGIN BASE COUNT REFERENCE SOURCE DEFINITION RESULT FEATURES TITLE Query Match 57.7%; Best Local Similarity 64.0%; JOURNAL Matches AUTHORS ORGANISM source 313 gaagctcctatactacatgtggaat 337 34 1 Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., R79758 yi89e12.rl Homo sapiens cDNA clone 146446 5'. Other ESTs: THC24005 Unpublished (1995) Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Hillier, L., Homo sapiens cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer $\{5'\}$ EST. R79758 NCBI gi: 611512 For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database Contact: Venter, JC Based Upon 52 Million Basepairs of cDNA Sequence Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Weidman, J.F., Li, Y., Bednarik, D.P., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., constructed by Bento Soares and M.Fatima Bonaldo. (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI Female placenta human clone=146446 library=Soares placenta Nb2HP vector=pT7T3D 932 Clopper Rd, Gaithersburg, MD 20878 The Institute for Genomic Research Initial Assessment of Human Gene Diversity and Expression Patterns Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; (tdbinfo@tdb.tigr.org). Email: tdbinfo@tdb.tigr.org Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 16; (bases 1 to 410) 107 3018699423 3018699056 Conservative b <1..>381 1..381 /note="human" /organism="Homo sapiens" Location/Qualifiers Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 78 c 410 bp Pred. No. 1.91e-02; Score 15; 0; 71 g Mismatches 125 t DB 70; Cao, L., Length 381; Indels Cepeda, M.A., 0; Marra, M., Gaps 0;

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Ş RESULT 맑 COMMENT ORIGIN FEATURES Tocas BASE COUNT COMMENT REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION Matches Query Match 57.7%; Best Local Similarity 63.0%; JOURNAL TITLE ORGANISM AUTHORS JOURNAL source 232 tccacttcgtacttctgtataggaact 258 6 tcctattcNNNNNNNngtataggaact 32 12 large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994) Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Arabidopsis thaliana rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA. Lambda PRIL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour darkthale cress clone=200C2T7 primer=T7 dye primer library=Lambda-PRL2 strain=var columbia vector=lambda Zip-Lox Rsitel=Sal Rsite2=Not H76310 H76310 412 bp mRNA EST 18015 Arabidopsis thaliana cDNA clone 200C2T7. NCBI gi: 856039 High quality sequence stops: Source: IMAGE Consortium, LLL Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Unpublished (1995) The WashU-Merck EST Project Wilson, R. Brassicaceae; Arabidopsis. primed cDNA. This clone is available royalty-free through LLNL; contact the Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, Michigan State University Contact: Thomas Newman Genes galore: a summary of methods for accessing results from Retzel, E. and Somerville, Email: est@watson.wustl.edu MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E. MSU-DOE Plant Research Laboratory Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales; inserts were directionally cloned with Sal-Not arms using oligo [MAGE Consortium (info@image.llnl.gov) for further information. (bases 1 to 412) 117 a 314 286 1800 Conservative /note="human" 1..410 /clone="146446" /organism="Homo sapiens" Location/Qualifiers 82 c = = = = Pred. No. 1.91e-02, Score 15; 0; 90 g Mismatches 277 118 t DB 56; 10; Length 410; 3 others Indels MO 63108 06-NOV-1995 <u>.</u> Gaps <u>.</u> 맠

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103 a<1..>412 /clone="200C2T7" /note="thale cress" /strain="var columbia" organism="Arabidopsis thaliana" ...412 ocation/Qualifiers 83 c 84 g

BASE COUNT Query Match 57.7%; Best Local Similarity 64.0%; Score 15; DB 101; Pred. No. 1.91e-02; 126 ~ Length 412; 16 others

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AC LT 13 AT31015 H76310; Arabidopsis thaliana 10-NOV-1995 (Rel. 45, Created) 10-NOV-1995 (Rel. 45, Last upd 10-NOV-1995 (Rel. 45, Last updated, Version 1) 18015 Arabidopsis thaliana cDNA clone 200C2T7. standard; RNA; EST; 412 BP.

Dilleniidae; Capparales; Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida; Brassicaceae

Newman T., de Bruijn F.J., Retzel E., Somerville C.; McIntosh L., Ohlrogge J., Raikhel N., Green P., Keegstra K., Kende H.,

Somerville S.,

Thomashow M.,

large-scale partial sequencing of anonymous Arabidopsis cDNA "Genes galore: a summary of methods for accessing results from

clones";

Plant Physiol. 106:1241-1255(1994).

State University MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu. NCBI gi: 1053561 Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan

Location/Qualifiers

source /organism="Arabidopsis thaliana"
/clone="200C2T7" 1..412

/note="thale cress" /strain="var columbia"

ERNA Sequence 412 BP; 103 A; 83 C; 84 G; 126 T; 16 other;

Query Match Best Local Similarity 64.0%; 16; Conservative 57.7%; Pred. No. 1.91e-02; Score 15; ç Mismatches DB 109; 9 Length 412; Indels 0 Gaps

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190 atacattacaaagaacaggaacttc 214

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KEYWORDS DEFINITION rocus RESULT SOURCE ACCESSION 14 T86566 yd77q07.rl Homo sapiens cDNA clone 114300 5' similar to SP:UBC5_DROME P35128 UBIQUITIN-CONJUGATING ENZYME E2-17 KD vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3EST. human clone=114300 library=Soares fetal liver spleen 1NFLS T86566 vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI contains Alu repetitive element;. 448 bp 17-MAR-1995

ORGANISM Homo sapiens

REFERENCE Eutheria; Primates; Catarrhini; Hominidae; lucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; (bases 1 to 448) Homo.

AUTHORS Hillier, L., Clark, N., Dubuque, T., Wilson, R. Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Elliston, K., Hawkins, M.,

TITLE JOURNAL Unpublished The WashU-Merck EST Project Unpublished (1995)

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK ⊡mail: est@watson.wustl.edu Fax: 314 286 1810 314 286 1800

Source: IMAGE Consortium, LLNL MAGE Consortium (info@image.llnl.gov) for further information. This clone is available royalty-free through LLNL; contact the

High quality sequence stops: 426

FEATURES source NCBI gi: 714918 /organism="Homo sapiens" /clone="114300" Location/Qualifiers

ORIGIN BASE COUNT 110 ø /note="human" 123 c 97 Q 114 t 4 others

Ş В Query Match 57.7%; Best Local Similarity 62.1%; Matches 414 gttccttttgtgatttctgtatagggact 442 4 gttcctattcNNNNNNnnnngtataggaact 32 18; Conservative Score 15; Pred. No. **.** Mismatches No. 1.91e-02; DB 85; 11; Length 448; Indels <u>.</u> Gaps

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RESULT LOCUS 15 T43599 452 유 ERNA S 17-AUG-1995

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RECCOSE DIDI S 밁 ORIGIN FEATURES COMMENT REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION BASE COUNT TITLE Matches Query Match 57.7%; Best Local Similarity 64.5%; AUTHORS ORGANISM JOURNAL AT5996 source Dilleniidae; Capparales; Brassicaceae Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida; Arabidopsis thaliana 6862 Arabidopsis thaliana cDNA clone 121G9T7. 03-FEB-1995 T43599; 03-FEB-1995 (Rel. 42, Created) 10-NOV-1995 (Rel. 45, Last upd 19 w agttcctattcNNNNNNngtataggaactt 33 agttgctattctntctactggagatgaactt 49 Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. thale cress clone=121G9T7 library=Lambda-PRL2 strain=var columbia vector=lambda Zip-Lox primer=T7 dye primer Rsite1=Sal Rsite2=Not Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated EST NCBI gi: T43599 Tel: 517-353-0854 Fax: 517-353-9168 Plant Physiol. 106, Genes galore: a summary of methods for accessing results from Arabidopsis thaliana rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA with 24 hour light cycle, half on 16 hr light, 8 hour darkseedlings; 2) tissue culture grown roots; 3) staged plants half 6862 Arabidopsis thaliana cDNA clone 121G9T7. Email: 22313tcn@ibm.cl.msu.edu. MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E. Michigan State University Contact: Thomas Newman Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales; primed cDNA. inserts were directionally cloned with Sal-Not arms using oligo dT Lansing, Mi MSU-DOE Plant Research Laboratory large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994) Brassicaceae; Arabidopsis. 20; (bases 1 to 452) 116 a standard; RNA; EST; 452 BP Conservative 947993 /note="thale cress" 69 c 115 g /organism="Arabidopsis thaliana" /strain="var columbia" /clone="121G9T7" 1...452 Location/Qualifiers Last updated, Version 8) Score 15; DB 74; Pred. No. 1.91e-02; <u>,,</u> Mismatches 130 ~ 11; Length 452; 22 others Indels 0; Gaps 0;

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Ş B REFERENCE KEYWORDS ACCESSION DEFINITION POCUS RESULT ORGANISM Matches Query Match 57.7%; Best Local Similarity 64.5%; JOURNAL AUTHORS Sequence 452 Key clones"; Newman T., source Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu. NCBI gi: 947993 State University MSU-DOE-PRL, Michigan State University,Plant Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan AGIS; T43599; AGIS July 1995. Plant Physiol. 106:1241-1255(1994). large-scale partial sequencing of anonymous Arabidopsis cDNA Retzel E., Somerville C., McIntosh L., *Genes galore: a summary of methods for accessing results from 19 agttgctattctntctactggagatgaactt 49 3 agttcctattcNNNNNNNgtataggaactt 33 17 Homo sapiens Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima yg83b07.rl Homo R53335 R53335 Contact: Wilson RK WashU-Merck EST Project Hillier, L., Clark, N., Dubuque, T., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; EST. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Unpublished Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Bonaldo. Rsite2=Hind III Whole brain from a 73 days post natal female. 1st GDB: G00-412-467 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Eutheria; Archonta; Primates; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; cDNA was ligated to Hind III adaptors (Pharmacia), digested with strand cDNA was primed with a Not I - oligo(dT) host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I human clone=39926 library=Soares infant brain INIB vector=Lafmid BA The WashU-Merck EST Project dilson, R. 20; (bases 1 to 469) de Bruijn F.J., Conservative BP; 116 A; 69 C; 115 G; 130 T; 22 other; Ohlrogge J., Raikhel N., /organism="Arabidopsis thaliana" /strain="var columbia" /clone="121G9T7" Location/Qualifiers note="thale cress" (1995) 469 bp sapiens _ _ _ _ _ _ _ Score 15; DB 110; Pred. No. 1.91e-02; Green P., Keegstra K., Kende H., 0; Mismatches 11; Indels cDNA clone 39926 mRNA Catarrhini; Hominidae; Homo. Somerville S., Elliston, K., Hawkins, M., S' Length 452; Thomashow primer [5']; double-stranded 18-MAY-1995 9 Gaps 3 <u>.</u>

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Best Local Similarity 64.0%;
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                                                                         Tel:
                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                  Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
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                                                                                                                                               WashU-Merck EST Project
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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394 ttcctatgcttctgggtgaatagga 418

Matches

16;

Conservative

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Mismatches

9;

Indels

0;

Gaps

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mRNA BASE COUNT ဌ В May 14 13:59 ORIGIN FEATURES Query Match 57.7%; Best Local Similarity 64.0%; Matches Query Match 57.7%; Best Local Similarity 64.0%; 21-OCT-1995 (Rel. 45, Last updated, Version 1) yul8g03.rl Homo sapiens cDNA clone 234196 5' similar to gb:S52450 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN);. Sequence 487 BP; 140 A; 93 C; 109 G; 144 T; 1 other; **BNA** Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: HS258215 source source est@watson.wustl.edu High quality sequence stops: 379 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL Unpublished Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Homo sapiens (human) 21-0CT-1995 H66258; "The WashU-Merck EST Project"; Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; 394 ttcctatgcttctgggtgaatagga 418 nformation. NCBI gi: 1024998 contact the IMAGE Consortium (info@image.llnl.gov) for further 30 ttcctatacNNNNNNNngaatagga 6 NCBI gi: 1024998 Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information. 16; standard; RNA; EST; 487 140 (Rel. Conservative മ IMAGE Consortium, <1..>487 /organism="Homo/clone="234196" 1..487 <1..>487 /note="human" Location/Qualifiers /note="human" /clone="234196" 1..487 /organism="Homo sapiens" Location/Qualifiers 93 c Created) Score 15; DB 116; Pred. No. 1.91e-02; Score 15; DB 98; Pred. No. 1.91e-02; <u>,</u>, 109 Mismatches 9 ВP FIP1st 144 t Length 487; Length 487; Indels others St. Louis, 0; Gaps 0

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KEYWORDS DEFINITION Tocas

SOURCE ACCESSION

ORGANISM

COMMENT

JOURNAL

REFERENCE

AUTHORS

TITLE

May 14 13:59

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FLP.rst

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Query Match 53.8%; Best Local Similarity 58.1%; HSGS04157 standard; RNA; EST; 138 BP.
p25789;
23-JUN-1994 (Rel. 40, Created)
27-NOV-1995 (Rel. 45, Last updated, Version 2)
Human colon 3'directed Mbol cDNA, HUMGS04157, clone cm1934. Okubo K., Yoshii J., Yokouchi H., Kameyama M., Okubo K., Itoh K., Yoshii J., Yokouchi H., Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae colon; endothel; EST(expressed sequence tag); gene signature(GS). Unpublished. random cDNA sequencing analysis"; Homo sapiens (human) Okubo K., Itoh K., Yoshii J., Yokouchi H., Matsubara K.; "Global analysis of gene expression in colon mucosa: a large scale 30 ttcctatacNNNNNNNngaatagga 3 agttcctattcNNNNNNNgtataggaactt 33 agttctnattcatttgaataaaaaggaactt 128 Homo sapiens Unpublished (1993) Global analysis of gene expression in colon mucosa: a large scale Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K. EST (expressed sequence tag); colon; endothel; gene signature(GS) Human colon 3'directed MboI cDNA, HUMGS04157, clone cm1934. HUMGS04157 NCBI gi: Fax : 06-875-1922. Phone: 06-877-5111 Suita, Osaka, 565 Osaka University Submitted (22-Nov-1993) to DDBJ by: Kousaku Okubo random cDNA sequencing analysis Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Homo sapiens male adult colon mucosa cDNA to mRNA. Eutheria; Primates; Haplorhini; Catarrhini; Hominidae 18; Institute for Molecular and Cellular Biology (bases 1 to 138) Yamadaoka 45 a Conservative 500472 /sequenced_mol="cDNA to mRNA"
/sex="male" /tissue_type="colon mucosa" 23 c 28 g 36 t 1..138 /organism="Homo sapiens" Location/Qualifiers /dev_stage="adult" 138 bp Score 14; DB 32; Pred. No. 3.47e-01; 0; Mismatches g 13; Length 138, Matsubara 6 others Indels <u>.</u>.. 18-JUN-1994 <u>.</u> Gaps 0 밁

BASE COUNT

FEATURES

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1-138

98 agttctnattcatttgaataaaaaggaactt 128

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Query Match 53.8%;
Best Local Similarity 58.1%;
Matches 18; Conservative
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Best Local Similarity 58.1%;
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Suita, Osaka, 565 Japan Phone: 06-877-5111 Fax : 06-875-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-Nov-1993) to DDBJ by: Kousaku Okubo Institute for
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Phone: 06-877-5111
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BP; 45 A; 23 C; 28 G; 36 T; 6 other;
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                                                                                       /tissue_type="colon mucosa"
23 c 28 g 36 t
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/dev_stage="adult"
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/sex="male"
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Pred. No. 3.47e-01;
                  Score 14; DB 32;
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DEFINITION POCAR S В ORIGIN BASE COUNT FEATURES COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION **FOCUS** RESULT එ KEYWORDS ACCESS ION RESULT Query Match 53.8%; Best Local Similarity 57.7%; AUTHORS ORGANISM JOURNAL source 96 ctnttcaagaaccagtntgggaactt 121 32 œ 24 23 agttcctatacNNNNNNNNngaataggaactt 2 ctattcNNNNNNNgtataggaactt 33 H07743 1 (bases 1 to 162)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. yb47e03.s1 Homo sapiens cDNA clone 74332 3' 40S RIBOSOMAL PROTEIN S18 (HUMAN). EST. EST. rape library=BNL1 strain=cv. Naehan vector=pT7T3D host=NM522 primer=M13 forward Rsitel=NotI Rsite2=EcoRI Poly(A)-mRNA was NCBI gi: 657167 High qality sequence starts: 1 High qality sequence stops: 1 Tel: 314 286 1800 Fax: 314 286 1810 Unpublished (1995) WashU-Merck EST Project Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens primer=-21m13 Rsite1=EcoRI Rsite2=XhoI Pooled fetal spleens. Cloned human clone=74332 library=Stratagene fetal spleen (#937205) khkh116 Source: IMAGE Consortium, LINI
This clone is available royalty free through LINI; contact the Email: est@watson.wustl.edu 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTT-3' Uni-ZAP XR Vector; vector=pBluescript SK- host=SOLR cells (kanamycin resistant) H07743 15; unidirectionally. IMAGE Consortium (info@image.llnl.gov) for further information. ۲ Conservative Brassica napus ø /note="human' /clone="74332" /organism="Homo sapiens" 1..162Location/Qualifiers 37 c ģ Primer: Oligo dT. Average insert size: 1.0 kb;
5' adaptor sequence: 5'-GAATTCGGCACGAG-3'; 3' Score 14; DB 77; Pred. No. 3.47e-01; <u>.</u> 32 g CDNA 3'. BRA Mismatches 49 t Length 162; EST 13 others similar to gb:X69150 08-FEB-1995 <u>.</u> <u>.</u>

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23

directionally cloned from the NotI site in the vector pT7T3D purified from constructed from (Pharmacia) to the EcoRI site. the the mRNAs leaf of B.napus. by oligo(dT) priming cDNA library and

ORGANISM Brassica napus Capparales; Brassicaceae; Brassica. Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Dilleniidae;

REFERENCE JOURNAL AUTHORS Unpublished (1995) Sohn, U., Lee, C.M., Cho, K.H., Jeon, Y.H., Hahn, T.R. and Nam, H.G (bases 1 to 226)

COMMENT

Fax: 0539555327 Tel: Contact: Uik Sohn EST is putatively homologous to Email: usohn@bh.kyungpook.ac.kr Kyungpook National University Laboratory of Molecular Biology . of Genetic Eng.,Kyungpook National Univ.,Taegu 702-701,Korea 0539505382 unknown gene.

ORIGIN BASE COUNT FEATURES source NCBI gi: 872565 61 മ /strain="cv. Naehan" /note="rape" 1..226 /organism="Brassica napus" Location/Qualifiers 45 c 66 g 54

£ 뭉 Matches Query Match 53.8%; Best Local Similarity 58.8%; 130 gaagttcccagacttcagttcgagttagaacctc 163 34 gaagttcctatacNNNNNNNngaataggaacttc 1 20; Conservative Score 14; DB 6; Pred. No. 3.47e-01 <u>.</u> Mismatches 14; Length 226; Indels 0 Gaps 9

15-NOV-1995 (Rel. 45, Created)
15-NOV-1995 (Rel. 45, Last updated, Version 1)
yu86e09.s1 Homo sapiens cDNA clone 240712 3' similar to gb:L11244
C4B-BINDING PROTEIN BETA CHAIN PRECURSOR (HUMAN);. н78142; HS142226 Homo sapiens (human) standard; RNA; EST; 240 BP.

Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Hominidae

Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., 1-240

Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;

"The WashU-Merck EST Project";

School of Medicine 4444 Forest Park Parkway, Box 85 MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Unpublished.

est@watson.wustl.edu High quality sequence stops: 59 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Key

Location/Qualifiers

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REFERENCE AUTHORS Ş 뮹 SO FITTER FR **LOCUS** FEATURES SOURCE KEYWORDS RESULT COMMENT ACCESSION DEFINITION Matches Query Match 53.8%; Best Local Similarity 61.8%; Query Match ORGANISM JOURNAL source Sequence 240 BP; 54 A; 58 C; 44 G; 71 T; 13 other; 178 gaagtgccttctcanactctggtttgggagcttc 211 26 gaagttcctattcNNNNNNNngtataggaacttc 34 yu10e03.s1 Homo sapiens cDNA clone 233404 3' similar to gb|M87942|HUMAALU83 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:X62078 GANGLIOSIDE GM2 ACTIVATOR PRECURSOR Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT^TT^3 vector. Library went through one round of normalization. Library Homo sapiens human clone=233404 primer=Promega -21m13 library=Soares fetal liver H79813 WashU-Merck EST Project Contact: Wilson RK Unpublished (1995) Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; constructed by Bento Soares and M.Fatima Bonaldo. and spleen from a 20 week-post conception male fetus. 1st strand host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker NCBI gi: 1057902 High quality sequence stops: 231 Tel: Washington University School of Medicine The WashU-Merck EST Project Wilson, R. Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; (HUMAN); contains Alu repetitive element;. This clone is available royalty-free through LLNL ; contact the Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu ax: 314 286 1810 MAGE Consortium (info@image.llnl.gov) for further information. (bases 1 to 265) Forest Park Parkway, Box 8501, St. Louis, 314 286 1800 Conservative <1..>240 /organism="Homo sapiens" /clone="240712" /note="human" Location/Qualifiers Score 14; DB 114; Pred. No. 3.47e-01; 0; Mismatches 13; DB 114; Length 240; Indels 0; MO 63108 09-NOV-1995 Gaps 0

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Best Local Similarity 61.5%;
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                                                                                                186 cctattcttgcacaggaataggacct 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector=Lafmid BA host=E. coli primer=M13 Forward (Universal)
Rsite1=Not I Rsite2=Hind III Size-selected cDNA from polyA+ RNA
from human brain. 3-month old meonate.This library is the result of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
                                                                                                                                                                                                                                                                                                                    NCBI gi: 471389
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Construction and characterization of a normalized cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Efstratiadis, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Psychiatry, 722 W 168th Street, Unit #41, New York, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                          Columbia University
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Similarity 68.2%;
                                                                                                                                                                                                                                                                                                                                                    Email: cuc@cuccfa.ccc.columbia.edu
                                                                                                                                                                                                                                                                                                                                                                       Fax: 2127955886
                                                                                                                                                                                                                                                                                                                                                                                        Tel: 2129602313
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SOURCE Pocus S 밁 FEATURES COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION SOURCE KEYWORDS ACCESSION DEFINITION RESULT ORIGIN BASE COUNT uery Match 53.8%; Best Local Similarity 59.4%; AUTHORS ORGANISM ORGANISM Matches JOURNAL source 254 aaattcctaatctgttttttctatagggcctt 285 2 aagttcctattcNNNNNNNgtataggaactt 33 မွ Parsons,J., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Wash-Merck EST Project G11665 Homo sapiens EST. T98116 ye30b04.rl Homo sapiens Homo sapiens 4444 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: vector=pBluescript SK- host=SOLR cells (kanamycin resistant) G11665 human STS WI-10042. NCBI gi: 747461 Tel: Unpublished (1995) primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72 human clone=119215 library=Stratagene lung (#937210) repetitive element ;. Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; human STSs derived from random genomic DNA. STS sequence; primer; sequence tagged site. This clone is available royalty-free through LLNL; contact the Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK 5'-GAATTCGGCACGAG-3'; 3' adaptor sequence: Catarrhini; Hominidae; Homo. 19; IMAGE Consortium (info@image.llnl.gov) for further information. Source: IMAGE Consortium, LLNL High quality sequence stops: mail: est@watson.wustl.edu Sutheria; Primates; Catarrhini; Hominidae; Sucaryotae; Metazoa; Chordata; Vertebrata; 5'-CTCGAGTTTTTTTTTTTTTTTTT-3'. (bases 1 to 309) 314 286 1810 88 314 286 1800 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Conservative a /note="human" /organism="Homo sapiens" /clone="119215" 1..309 Location/Qualifiers 75 c 326 bp Score 14; DB 88; Pred. No. 3.47e-01 <u>.</u>. 35 cDNA clone 119215 5' similar to DNA Mismatches 9 110 t Length 309; STS 1 others Gnathostomata; Mammalia; Homo. Indels 19-0CT-1995 0 Gaps contains 9 드

REFERENCE

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Whitehead Institute/MIT Center for Genome Research; Physically

AUTHORS TITLE

Hudson, T.

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REFERENCE TOCUS FEATURES COMMENT REFERENCE SOURCE KEYWORDS SOURCE KEYWORDS DEFINITION RESULT BASE COUNT ACCESSION ACCESSION Query Match 53.8%; Best Local Similarity 58.8%; JOURNAL AUTHORS ORGANISM Matches JOURNAL AUTHORS ORGANISM source 203 gaagtgccttctcacactctggtttgggagcttc 236 1 gaagttcctattcNNNNNNNngtataggaacttc 34 32 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project
Unpublished (1995) Arabidopsis thaliana Primer: Oligo dT. Hepatectomy from normal 49 year old male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGCACGAG-3'; 3' adaptor sequence: human clone=61440 library=Stratagene liver (#937224) vector=pBluescript SK host=SOLR cells (kanamycin resistant) primer=-21ml3 Rsite1=EcoRI Rsite2=KhoI Cloned unidirectionally. EST. SP:C4BB HUMAN P20851 C4B-BINDING PROTEIN BETA CHAIN ,. T40922 Homo sapiens Direct Submission Submitted (15-SEP-1994) to the EMBL/GenBank/DDBJ databases. Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; thale cress. A. thaliana transcribed sequence; clone FAFM89 Other_ESTs: yal4c01.r2 Unpublished (1995) Parmentier, Y., Criqui, M.C., Durr, A. and Fleck, J. expressed sequence tag; partial cDNA sequence Z37189 ATTS3932 NCBI gi: 648505 5'-CTCGAGTTTTTTTTTTTTTTTTT-3'. Magmoliopsida; Dilleniidae; Capparales; Brassicaceae; Arabidopsis. 20; This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Source: IMAGE Consortium, LLNL ⊡mail: est@watson.wustl.edu Tel: 314 286 1800 Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Sutheria; Primates; Catarrhini; Hominidae; Sucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; (bases 1 to 347) 84 Conservative D) /note="human" 1..345 /organism="Homo sapiens" Location/Qualifiers /clone="61440" 89 c 347 bp Pred. No. 3.47e-01; Score 14; 0; Mismatches 6 RNA Ω DB 73; Length 345; 112 t EST Homo. Indels 16-SEP-1994 0; Gaps 0

GDR-1003 ACS, INRA, laboratoire de Biologie Moleculaire,

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Best Local Similarity 61.5%;
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                                                                                     Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                            Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8,
                                                                                                                                                                                                                                                                                                                                         Submitted (19-JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail:fleck@scilla.u-strasbg.fr
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                                                                  Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                           Genexpress.
                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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                                             IMAGE: Integated molecular analysis of the human genome and
                                                                                                                                                                                Unpublished
                                                                                                                                                                                                     The Genexpress cDNA program
                                                                                                                                                                                                                                                                         Villejuif Cedex France. E-mail: genexpress@genethon.fr
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/clone="FAFM89"
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Sci. Vie 318, 263-272 (1995)
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Best Local Similarity 60.0%;
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27-AUG-1995
                                                  source
                                                                                                                                       Submitted (30-May-1995) to DDBJ by: Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 kagasuno
                                                                                                                                                                                                                                           Fujiwara T., Hirano H., Katagiri T., Kawai A., Kuga Y., Nagata M.,
Okuno S., Ozaki K., Shimizu F., Shimada Y., Shinomiya H.,
                                                                                                                                                                                                                                                                                                            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Theria; Eutheria; Primates; Haplorhini; Catarrhini;
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                                                                                                                       Kawauchi-cho Tokushima, Tokushima 771-01 Japan Phone: 0886-65-2888
                                                                                                                                                                           Unpublished.
                                                                                                                                                                                        Maekawa H., Shin S., Nakamura Y.;
*Unpublished(101)*;
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                  similar to none (May 29, 1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 45, Created)
(Rel. 45, Last upd
                                                                                                                                                                                                                         Takeda S., Watanabe T., Takahashi E.i., Hirai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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88 c 83 g 75 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="normalized infant brain cDNA from Psychiatry Dept. Columbia University USA"
/sequenced_mol="cDNA to mRNA"
/clone_lib="Clontech human fetal brain polyA+ mRNA (#6535)
                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="total brain"
/dev_stage="3 months old"
                                                                                    Location/Qualifiers
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Pred. No. 3.47e-01
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Sequence 369 BP; 154 A; 57 C; 59 G; 90 T; 9 other;

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Matches
                  Query Match 53.8%;
Best Local Similarity 60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                           NCBI gi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I and cloned into the Not I and Eco RI sites of the modified pT7T3
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18;
                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
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                                                                                                                                   /note="human"
                                                                                                                                                      /organism="Homo sapiens"
/clone="141596"
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                  Score 14; DB 53;
Pred. No. 3.47e-01;
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Best Local Similarity 59.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                         NCBI gi: 783973
                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 314 286 1810
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/clone="134647"
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Pred. No. 3.47e-01
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Best Local Similarity 62.5%;
Matches 15; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                        275 tccaatactacagaatgaatagga 298
                                                                                                                                                                                                                           29
                                                                                                                                                    38
                                                                                                                                                                                                                           tcctatacNNNNNNNngaatagga 6
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yf39q03.rl Homo sapiens cDNA clone 129268 5' similar to SP:TOA2_YEAST P32774 TRANSCRIPTION INITIATION FACTOR IIA SMALL
                                                                         yh58f05.s1 Homo sapiens cDNA clone 133953 3'. R28016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                             R28016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI gi: 763854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I and cloned into the Pac I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strand cDNA was primed with a Pac I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human clone=129268 library=Soares fetal liver spleen 1NFLS
                      human clone=133953 library=Soares placenta Nb2HP vector=pT7T3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stops: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liver and spleen from a 20 week-post conception male fetus. 1st
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="129268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 c
                                                                                                                         418 bp
                                                                                                                                                                                                                                                      =
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                                                                                                                                                                                                                                                                                                                                               Score 14; DB 36;
Pred. No. 3.47e-01;
                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 g
                                                                                                                             ERNA
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                        Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 others
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                             25-APR-1995
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                                                                                                                                                                                                                                                                                                                             Gaps
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May 14 13:59 FLP1st

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cDNA was ligated to Eco RI adaptors (Pharmacia), placenta obtained at birth (full term). 1st strand cDNA was primed I and cloned into the Not I and Eco RI sites of the modified pT7T3 with a Not I - oligo(dT) primer [5' resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Female digested with Not

ORGANISM Homo sapiens

Eutheria; Primates; Catarrhini; Hominidae; Homo. Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

constructed by Bento Soares and M.Fatima Bonaldo.

vector. Library went through one round of normalization. Library

REFERENCE (bases 1 to 418)

AUTHORS Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

JOURNAL Unpublished (1995) The WashU-Merck EST Project

COMMENT

WashU-Merck EST Project Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

314 286 1800

Email: est@watson.wustl.edu

Source: IMAGE Consortium, LLNL High quality sequence stops:

[MAGE Consortium (info@image.llnl.gov) This clone is available royalty-free through LLNL; contact the ior further information.

NCBI gi: 784151

FEATURES source ..418 Location/Qualifiers

/organism="Homo sapiens" /clone="133953"

132 ø /note="human" 60 c 85 g 137 t 4 others

ORIGIN BASE COUNT

Matches Query Match 53.8%; Best Local Similarity 60.0%; 18; Conservative Score 14; DB 41; Pred. No. 3.47e-01 Mismatches DB 41; Length 418; Indels <u>.</u> Gaps

0

167 gaagttettattgtaeatgtageatgggaa 196 ||||||| |||

1 gaagttcctattcNNNNNNngtataggaa 30

KEYWORDS ACCESSION DEFINITION POCO S RESULT SOURCE 39 ye81a01.s1 Homo sapiens cDNA clone 124104 3'. R01221 EST. R01221 421 bp BRNA

vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=-21ml3 Rsite1=Pac I Rsite2=Eco RI human clone=124104 library=Soares fetal liver spleen Library went through one round of normalization. Library

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Ş 망 KEYWORDS COMMENT SOURCE **FOCUS** RESULT ORIGIN BASE COUNT FEATURES REFERENCE ACCESSION DEFINITION ORGANISM ORGANISM Matches Best Local Similarity Query Match JOURNAL AUTHORS source 255 ttnctattcattctgtagtattgga 279 5 ttcctattcNNNNNNngtatagga 29 40 yd35c09.r1 Homo sapiens cDNA clone 110224 5' similar to gb|L13707|HUM5CALUE Human scRNA molecule, transcribed from Alu (rRNA); gb:J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);contains Alu Contact: Wilson RK WashU-Merck EST Project Hillier, L., Clark, N., Dubuque, T., Homo sapiens Homo sapiens repetitive element;. T71405 NCBI gi: High quality sequence stops: 361 Tel: Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Unpublished (1995) The WashU-Merck EST Project Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Eutheria; Primates; Eucaryotae; Metazoa; constructed by Bento Soares and M.Fatima Bonaldo vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B human clone=110224 library=Soares fetal liver spleen INFLS Email: est@watson.wustl.edu Holman, M., Hultman, M., Eutheria; Primates; Catarrhini; Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; constructed by Bento Soares and M.Fatima Bonaldo. vector. Library went through one round of normalization. I and cloned into the Pac I and Eco RI sites of the modified pT7T3 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac strand cDNA was primed with a Pac I - oligo(dT) primer [5' IMAGE Consortium (info@image.llnl.gov) for further information. This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL Liver and spleen from a 20 week-post conception male fetus. 1st (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI 15; (bases 1 to 421) 129 314 286 1810 314 286 1800 Conservative b 750957 1..421 /clone="124104" /note="human" /organism="Homo sapiens" Location/Qualifiers 53.8%; 60.0%; 72 c Catarrhini; Chordata; Pred. No. 3.47e-01 Score 14; <u>,</u>. 74 g Kucaba, T., Le, M., Lennon, G., Marra, M., Mismatches 142 t Vertebrata; DB 34; Length 421; Hominidae; Hominidae; Elliston, K., Hawkins, M., 10; 4 others Indels Ното. Gnathostomata; Mammalia; MO 63108 15-MAR-1995 ç Gaps Library ç

May 14:13:59 FLP.rst
REFERENCE 1 (bases 1 to 450)

36

COMMENT AUTHORS JOURNAL Tel: 314 286 1800 Fax: 314 286 1810 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Other_ESTs: yd35c09.s1 Unpublished (1995) Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., NCBI gi: Source: IMAGE Consortium, LLNL High qality sequence stops: 327 WashU-Merck EST Project Contact: Wilson RK The WashU-Merck EST Project Wilson, R. This clone is available royalty-free through LLNL; contact the Email: est@watson.wustl.edu Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and IMAGE Consortium (info@image.llnl.gov) for further information. (bases 1 to 450) 685926 MO 63108

Ş 밁 ORIGIN BASE COUNT FEATURES Matches Query Match 53.8%; Best Local Similarity 62.5%; source 145 attctttatttggtattggaactt 168 10 attcNNNNNNNngtataggaactt 33 15; 111 Conservative b /note="human" /organism="Homo sapiens" /clone="110224" Location/Qualifiers = = = = 93 c Pred. No. 3.47e-01; Score 14; 110 g ۰, Mismatches 133 t DB 81; Length 450; 9; Indels 3 others ç Gaps

0

KEYWORDS ACCESSION DEFINITION rocas 41 yp24g12.s1 Homo sapiens cDNA clone 188422 3' H44838 digested with Not I and cloned into the Not I and Eco RI sites of of normalization to a Cot = 20. Library constructed by Bento Soares modified pT7T3 vector (Pharmacia). Library went through one round double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), resistant) primer=Promega -21ml3 Rsite1=Not I Rsite2=Eco RI Adult and M.Fatima Bonaldo. (Pharmacia) with a modified polylinker host=DH10B (ampicillin human clone=188422 library=Soares breast 3NbHBst vector=pT7T3D numan. 1st strand cDNA was primed with a Not I - oligo(dT) primer

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Osteichthyes;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 468)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Patrsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

37

The WashU-Merck EST Project

RESULT COMMENT REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION TOCUS Q В ORIGIN BASE COUNT FEATURES COMMENT AUTHORS ORGANISM Matches Query Match 53.8%; Best Local Similarity 60.7%; JOURNAL JOURNAL source 65 7 cctattcNNNNNNNgtataggaacttc 34 42 cccattccagcctgcttattggaacttc 92 yb27g03.sl Homo sapiens cDNA clone 72436 3'. T51605 Tel: Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Hillier, L., Homo sapiens unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGCACGAC-3'; 3' EST. Unpublished (1995) High qality sequence stops: 380 Unpublished (1995) Waterston, R., Williamson, A., WashU-Merck EST Project primer=-21m13 Rsite1=EcoRI Rsite2=KhoI Pooled fetal spleens. Cloned 17; NCBI gi: This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, High quality sequence stops: 345 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK vector=pBluescript SK- host=SOLR cells (kanamycin resistant) human clone=72436 library=Stratagene fetal spleen (#937205) Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Email: est@watson.wustl.edu Eutheria; Primates; Catarrhini; Hominidae; Homo. Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTT-3'. IMAGE Consortium (info@image.llnl.gov) for further information. Email: est@watson.wustl.edu (bases 1 to 471) 121 314 286 1800 314 286 1800 Conservative ۵ 920890 /note="human" /clone="188422" /organism="Homo sapiens" 1..468 Location/Qualifiers Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 109 c 471 bp Score 14; DB 17; Pred. No. 3.47e-01; 101 g 0; Mismatches 133 t 11; Length 468, 4 others Indels 08-FEB-1995 0 Gaps 0,

> May 14 13:59 FIPs

> > 38

Source: IMAGE Consortium, warm
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information

FEATURES source NCBI gi: 653465 1..471Location/Qualifiers /organism="Homo sapiens"

ORIGIN BASE COUNT 143 Ŋ /note="human" /clone="72436" 81 c 95 g 150 t 2 others

င Query Match 53.8%; Best Local Similarity 59.4%; Matches 174 aagttcctctattattcatagaaaagaaattt 205 33 aagttcctatacNNNNNNNgaataggaactt 2 = = = = 19; Conservative = = = = Score 14; DB 76; Pred. No. 3.47e-01; 0; Mismatches Length 471; Indels 0; Gaps 0;

SOURCE KEYWORDS DEFINITION TOCUS. RESULT ACCESSION 3 representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13Rev Rsite1=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I -EST. yo09d08.r1 Homo sapiens cDNA clone 177423 5'. H42585 subcortical white matter, basal ganglia, thalamus, cerebellum, through one round of normalization to a Cot = 53. Library Homo sapiens clone=177423 library=Soares adult brain N2b5HB55Y H42585 midbrain, pons and medulla. constructed by Bento Soares and M.Fatima Bonaldo. The adult brain oligo(dT) primer [5' aortic aneurysm. RNA was prepared from a pool of tissues hours after death which occurred in consequence of a ruptured RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 RI sites of a modified pT7T3 vector (Pharmacia). Library went double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco 473 bp **PRNA**

REFERENCE ORGANISM Homo sapiens Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Osteichthyes; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; (bases 1 to 473) Catarrhini; Hominidae; Homo.

AUTHORS JOURNAL Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Unpublished (1995) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., WashU-Merck EST Project Contact: Wilson RK The WashU-Merck EST Project Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Holman, M., Hultman, M., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Kucaba, T., Le, M., Lennon, G., Marra, M.,

COMMENT

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Ş 맑 **TOCUS** RESULT FEATURES REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION BASE COUNT Query Match 53.8%; Best Local Similarity 60.7%; ORGANISM Matches JOURNAL AUTHORS source 136 gttcttattcatatatttttataggcac 163 4 gttcctattcNNNNNNNgtataggaac 31 44 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Ritkin, L., Rohlling, T., Soares, M., Tan, F., Homo sapiens cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3EST H01413 yi99cl0.rl Homo sapiens cDNA clone 147378 5'. Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Fax: 314 286 1810
Email: est@watson.wustl.edu Unpublished (1995) constructed by Bento Soares and M.Fatima Bonaldo. vector. Library went through one round of normalization. Library obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' H01413 NCBI gi: 918637 High quality sequence stops: 169 High qality sequence stops: 339 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta human clone=147378 library=Soares placenta Nb2HP vector=pT7T3D This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu Fax: 314 286 1810 Contact: Wilson RK Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and (Pharmacia) with a modified polylinker host=DH10B (ampicillin IMAGE Consortium (info@image.llnl.gov) for further information (bases 1 to 476) 119 314 286 1810 314 286 1800 Conservative /clone="177423" 1..473 /organism="Homo sapiens" Location/Qualifiers 79 c 476 bp Score 14; DB 16; Pred. No. 3.47e-01; Mismatches 98 g 162 t Length 473; 15 others Indels <u>.</u>. Gaps <u>,</u>

May 14 13:59 FLP.1st

8

င္ပ FEATURES COMMENT REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION RESULT ORIGIN BASE COUNT FEATURES Matches Query Match 53.8%; Best Local Similarity 65.4%; ORGANISM JOURNAL AUTHORS source source 386 gttcctatgcntattttttaatagga 411 31 gttcctatacNNNNNNNngaatagga 6 45 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. primer=-21m13 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAG-3'; 3' adaptor sequence: EST. yc13f05.sl Homo sapiens cDNA clone 80577 3' similar to NCBI gi: 864346 Unpublished (1995) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Homo sapiens vector=pBluescript SK- host=SOLR cells (kanamycin resistant) T59688 SUBUNIT (HUMAN);. gb:D90150 rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(2), ALPHA Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 5'-CTCGAGTTTTTTTTTTTTTTTT-3'. human clone=80577 library=Stratagene lung (#937210) T59688 NCBI gi: 661525 WashU-Merck EST Project Contact: Wilson RK WashU-Merck EST Project Eutheria; Primates; Catarrhini; Hominidae; MAGE Consortium (info@image.llnl.gov) for further information. This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL High qality sequence stops: 324 mail: est@watson.wustl.edu Fax: 314 286 1810 Sucaryotae; Metazoa; Chordata; Vertebrata; 17; (bases 1 to 516) 137 314 286 1800 Conservative a /note="human" /note="human" /clone="147378" /organism="Homo sapiens" 1..476 Location/Qualifiers /clone="80577" /organism="Homo sapiens" Location/Qualifiers 77 c 516 bp Score 14; DB 4; Pred. No. 3.47e-01 0; Mismatches 78 g 177 t Length 476; 9 Louis, MO 63108 7 others Gnathostomata; Mammalia; Indels Homo. 0; Gaps 0

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148

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151 t

5 others

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Set	Items	Description	
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S4	0	AU="O'GORMAN S?" AND FLP	510/
S5	1	FLP AND MICE	51
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Genetic regulation of mec-3 gene expression implicated in the specification of the mechanosensory neuron cell types in Caenorhabditis elegans

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Development Growth & Differentiation 37 (5). 1995. 551-557.

Full Journal Title: Development Growth & Differentiation

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FLP recombinase in transgenic plants: Constitutive activity in stably transformed tobacco and generation of marked cell clones in Arabidopsis Kilby N J; Davies G J; Snaith M R; Murray J A H

Inst. Biotechnol., Univ. Cambridge, Tennis Court Rd., Cambridge CB2 1QT, UK

Plant Journal 8 (5). 1995. 637-652.

Full Journal Title: Plant Journal

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Heat-inducible expression of FLP gene in maize cells Lyznik L A; Hirayama L; Rao K V; Abad A; Hodges T K

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Site-specific Transgene Insertion: An Approach

Wigley P; Becker C; Beltrame J; Blake T; Crocker L; Harrison S; Lyons I;

McKenzie Z; Tearle R; Crawford R; Robins A

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Reproduction Fertility and Development 6 (5). 1994. 585-588.

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11204786 BIOSIS Number: 97404786

A cell-autonomous, ubiquitous marker for the analysis of Drosophila genetic mosaics

Vincent J-P; Girdham C H; O'Farrell P H

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Developmental Biology 164 (1). 1994. 328-331.

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10922464 BIOSIS Number: 97122464

A new method for manipulating transgenes: Engineering heat tolerance in a complex, multicellular organism

Welte M A; Tetrault J M; Dellavalle R P; Lindquist S L

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Current Biology 3 (12). 1993. 842-853.

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ISSN: 0960-9822 Language: ENGLISH

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9042030 BIOSIS Number: 93027030

FLP-MEDIATED RECOMBINATION IN THE VECTOR MOSQUITO AEDES-AEGYPTI MORRIS A C; SCHAUB T L; JAMES A A

MORKID A C, SCHAOD I II, UAMED A A

DEP. MOL. BIOL. AND BIOCHEM., UNIV. CALIF., IRVINE, CALIF. 92717.

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Language: ENGLISH

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11521508 BIOSIS Number: 98121508

Site-specific Transgene Insertion: An Approach

Wigley P; Becker C; Beltrame J; Blake T; Crocker L; Harrison S; Lyons I;

McKenzie Z; Tearle R; Crawford R; Robins A

Bresatec Lab., Dep. Biochem., Univ. Adelaide, SA 5005, Australia

Reproduction Fertility and Development 6 (5). 1994. 585-588.

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Methods to improve the production of transgenic animals are being developed. Conventional transgenesis, involving microinjection of DNA into fertilized eggs, has a number of limitations. These result from the inability to control both the site of transgene insertion and the number of gene copies inserted. The approach described seeks to overcome these problems and to allow single copy insertion of transgenes into a defined site in animal genomes. The method involves the use of embryonic stem cells, gene targeting and the FLP recombinase system.

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8208682 BIOSIS Number: 91129682

RECOMBINASE-MEDIATED GENE ACTIVATION AND SITE-SPECIFIC INTEGRATION IN MAMMALIAN CELLS

O'GORMAN S; FOX D T; WAHL G M

GENE EXPRESSION LAB., SALK INST. BIOL. STUDIES, LA JOLLA, CALIF. 92037. SCIENCE (WASHINGTON D C) 251 (4999). 1991. 1351-1355. CODEN: SCIEA Full Journal Title: SCIENCE (Washington D C)

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3(prm1)TC5(prm1)) adjacent to the top-strand cleavage point. The unlabeled substrate was a concatemer of S2 obtained by self-ligation (S2n). S2 also contained two mismatched spacer positions next to the top-strand cleavage site (5(prm1)AG3(prm1)/3(prm1)AA5(prm1)). Following strand swapping between S1 and S2, the spacers would be fully matched (5(prm1)AG3(prm1)/3(prm1)TC5(prm1)) and 5(prm1)TT3(prm1)/3(prm1)AA5(prm1)). Strand cleavage and strand transfer products are designated CP and STP, respectively. S represents the substrate. The heterogeneity in strand transfer products results from the multiplicity of crossover points within S2n. For each reaction set with a complementing protein pair, the leftmost lane represents a reaction with the triad variant alone (at the same molar concentration as in the rightmost lane). The next three lanes represent reactions containing the triad variant and Flp(Y343F) in approximate molar ratios of 1:1, 1:1.5, and 1:2, respectively. Roughly 3 pmol of Flp(Y343F) was present per pmol of the Flp-binding element. Lane C represents an assay with no <u>Flp</u> or <u>Flp</u> variant added to the reaction. The <u>Flp</u> reaction shown in lane 2 contained S1 but not S2n. The product X likely arose by cleavage within S1 and subsequent phosphoryl transfer to the 5(prm1)-hydroxyl group of the unannealed top-strand oligodeoxynucleotide of S1 present in the reaction. The size of X, as measured against standard molecular size markers, fits this explanation. Note the presence of X in a reaction containing S1 alone (lane 2). WT, wild type.

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recombination by <u>Flp</u>, they do not allow us to distinguish among the three potential types of trans DNA cleavage, trans horizontal, trans vertical, and trans diagonal (6; Fig. 1A). Results obtained with half-site reactions tend to disfavor the trans-vertical mode, while distinction between the trans-horizontal and trans-diagonal modes is not possible. Our expressed preference for trans-diagonal cleavage (6) over trans-horizontal cleavage must be tempered by the possibility that half sites are likely to enjoy greater freedom of stacking interactions in solution over full sites (11; Fig. 1B). The critical question is: what is the cleavage mode in full-site recombination? The answer can be sought provided a tagged recombinase can be targeted to a specific binding arm within a full-site recombination complex.

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<u>Flp</u> assembles a functional active site from partial active sites during full-site recombination:

The apparent cis DNA cleavage by Int in full attB sites and Holliday junctions calls into question the pertinence of the active-site assembly by <u>Flp</u> during a half-site reaction to that during normal recombination. The design of full sites containing mismatched spacers has allowed us to address this issue directly. Complementation by step arrest variants of <u>Flp</u> to mediate strand cleavage in full sites supports the shared-active-site configuration during a normal recombination reaction. In a reaction carried out by a pair of <u>Flp</u> step arrest mutants, cleavage is executed by the protein partner harboring Tyr-343, thus virtually excluding the operation of an aberrant pathway during complementation.

Recently, mechanistic analyses of another Int family recombinase, Xer (responsible for stable chromosome partitioning in Escherichia coli), have become possible (5). Recombination in this system requires the combined action of two recombinases, XerC and XerD. The binding arms of the Xer target site encode specificities for each of the two protein monomers. The cleavage pattern observed with Xer is most easily explained by cis DNA cleavage, although one particular type of trans cleavage (trans vertical or partner trans; 6, 16) cannot be ruled out.

The (lambda) Int and Xer examples, contrasted with <u>Flp</u>, imply that Int family recombinases do not conform to the same rules in building their active sites. However, one suspects that, within the fully assembled active sites of these proteins, key catalytic residues must have the same relative spatial disposition. This would account for the fact that they follow the same chemistry of recombination. Global diversity and limited homology, which are the hallmarks of this family (3), would then make a strong case for mechanistic convergence (8, 16) among proteins that execute chemically identical reactions.

Which mode of trans cleavage does <u>Flp</u> follow?: While our results strongly support trans DNA cleavage during full-site

- FIG. 5. [GREY SCALE PLATE AVAILABLE] Complementation between $\underline{\text{Flp}}(Y343F)$ and double or triple triad mutants of $\underline{\text{Flp}}$ in full-site cleavage. The substrate was labeled at the 3(prm1) ends. The proteins used in the assays are indicated above the lanes. The substrate band (S) and the cleavage products (CL and CR) are labeled as in Fig. 3. A control reaction without $\underline{\text{Flp}}$ or $\underline{\text{Flp}}$ variants is shown in lane C.
- FIG. 6. [GREY SCALE PLATE AVAILABLE] Strand transfer in full sites by pairwise combinations of <u>Flp</u> step arrest mutants. The substrates used in the assay are schematically shown at the top. The labeled substrate S1 contained (sup32)P at the 3(prm1) end of the top strand and two spacer mismatches (5(prm1)TT3(prm1) and

3

The successful execution of strand exchange within a full site by a complementing pair of <u>Flp</u> variants fully corroborates the inference from half-site reactions that <u>Flp(Y343F)</u> (harboring an intact RHR triad) can facilitate not only strand cleavage but also strand joining by using a Tyr-343 residue and a 5(prm1)-hydroxyl group, respectively, donated in trans.

DISCUSSION

The partial-active-site-trans DNA cleavage model for <u>Flp</u> was first proposed to account for the pattern of DNA cleavage and strand transfer in half-site substrates by complementing

FIG. 3. [GREY SCALE PLATE AVAILABLE] Complementation between Flp(Y343F) and triad mutants of Flp in full-site substrates. The full site used in the assays is schematically represented at the top (Fig. 2). The parallel arrows represent the Flp-binding elements; the short vertical arrows indicate the points of strand cleavage by Flp. The two mismatched positions within the spacer adjacent to the cleavage sites are shown by the bubbles. DNA sequences unrelated to recombination are symbolized by the wavy lines. The asterisks stand for the (sup32)P label at the 3(prm1) ends. Products of cleavage from the top strand (left) and the bottom strand (right) are labeled CL and CR, respectively. The substrate band is designated S. The lane marked C is a reaction in which no Flp or Flp variant was added. WT, wild type.

FIG. 4. [GREY SCALE PLATE AVAILABLE] Identification of the protein partner responsible for strand cleavage during catalytic complementation. Strand cleavage assays were carried out by using the substrate used in reactions shown in Fig. 3. The radioactive label was placed at the 5(prm1) end of each strand (asterisks). The covalent DNA-protein complex resulting from strand cleavage by Flp (or a Flp variant) is called DPC; that derived from GST-Flp (or a GST-Flp variant) is called DPCG. The doublets corresponding to DPC or DPCG are most likely cleavage products derived from the top and bottom strands. The substrate DNA band is marked S. Flp and the Flp variants used in the reactions are indicated above the appropriate lanes. Lane C is a control reaction without added Flp or Flp variants. WT, wild type.

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pairs of catalytic <u>Flp</u> mutants (6, 7, 13). The validity of the model was then verified for the R recombinase from Z. rouxii in half-site strand transfer reactions (24). The simplicity and functional parsimony of the model led us to speculate that the rules of active-site assembly and of DNA cleavage are likely to extend beyond the yeast site-specific recombinases and encompass the entire Int family. Experiments with (lambda) Int and suicide attL, attB, or Holliday junction substrates have yielded rather paradoxical results (10, 16). While one set of results supports the <u>Flp</u> paradigm (10), the other set casts doubt on the generality of the model (16).

recombination could be kept hidden. However, difficulty in selectively binding a protein monomer to one of the two normal binding elements of the full-site substrate poses an impediment to the rigorous testing of this prediction. Nevertheless, the degree of cleavage reduction obtained upon the mixing of roughly equal amounts of <u>Flp</u> and <u>Flp(H305L, Y343F)</u> was consistent with inactivation of the wild-type partner in a double-mutant-wild-type protein pair (data not shown).

Strand transfer in bubbled full sites by pairwise combination of Flp(Y343F) and triad variants of Flp: According to the partial-active-site-trans-cleavage model, during complementation between a Flp triad mutant and Flp(Y343F), cleavage should occur on the scissile phosphodiester adjacent to the bound Flp(Y343F) (the cis configuration in Fig. 1A) and away from the triad mutant (the trans configuration in Fig. 1A) (6, Once the DNA 3(prm1)-phosphotyrosyl bond has been formed, Flp(Y343F) can facilitate the strand-joining reaction by using the 5(prm1)-hydroxyl group as the nucleophile (13, 17). In the bubbled full-site substrate, the spacer mismatch inhibits the joining reaction. However, if one used a pair of substrates (S1 and S2n in Fig. 6), each mismatched within its spacer but fully matched with the partner's spacer, strand joining within a substrate (parental mode) would be suppressed but that between partners (recombinant mode) would be encouraged. Even when the lack of a second pair of exchanges (as with a pair of complementing mutants) would tend to reverse this reaction, one might expect to trap some of the strand transfer product. With wild-type Flp, strand transfer products were formed from this pair of substrates (lane 3 in Fig. 6). The heterogeneity of strand transfer products results from the fact that one of the two DNA substrates (the nonradioactive one) was a concatemer of a single full site (S2) obtained by ligation. We resorted to this trick because, under our assay conditions, strand transfer efficiency was increased severalfold by increasing the length of at least one of the recombination partners. The size of the recombinant strand would depend on the site within S2n at which crossover occurred. In reactions containing Flp(Y343F) in combination with a triad single mutant or a triad double mutant, strand transfer was indeed detected (lanes 6 to 8, 10 to 12, 14 to 16, and 18 to 20 in Fig. 6). The low level of reaction compared with the wild type is not surprising. Since a single-strand transfer requires a matched pair of cleavage events within the two substrates (on the top strands or the bottom strands), only a reaction complex containing two appropriately positioned Flp(Y343F) and triad mutant monomers would be successful in completing an exchange event. Further, unlike, the wild-type reaction, the mutant pair reaction cannot execute the second pair of exchanges that yields the mature recombinant product. One would expect, therefore, that reversal of the first exchange (due to the absence of a second exchange) would be more pronounced in a reaction containing the complementing partners than in the wild-type reaction.

cleavage product corresponded in size to that obtained with GST-Flp (lane 9 in Fig. 4).

The pattern of DNA-protein adducts observed in the complementation reactions demonstrates that cleavage is carried out exclusively by the protein partner that harbors the active-site tyrosine. The simplest interpretation of the results is that it is indeed Tyr-343 that performs strand cleavage. The more complex scenario in which the active species is derived from the triad variant but is a surrogate nucleophile rather than Tyr-343 is not excluded. However, this possibility is strongly discounted by the fact that no complementation was obtained between Flp(Y343F) and a double variant altered at a triad position and Tyr-343 (data not shown).

The donor of Tyr-343 during catalytic complementation can be mutated at all triad positions: The shared-active-site model for Flp predicts that a Flp variant doubly or triply mutated in the RHR triad would be as competent as the single mutant in catalytic complementation with Flp(Y343F) provided their binding affinities for the target DNA do not differ significantly. This prediction has been verified in half-site recombination (7). We tested two triad double mutants and a triad triple mutant in combination with Flp(Y343F) in the cleavage assay with the bubbled full site (Fig. 5). Individually, neither the triad mutants nor Flp(Y343F) could effect strand cleavage (lanes 3, 4, 6, and 8 in Fig. 5). In contrast, each pair formed by mixing Flp(Y343F) and a triad mutant in roughly equimolar amounts exhibited approximately the same levels of complementation (lanes 5, 7, and 9 in Fig. 5). A second strong prediction of the partial-active-site model is that a triad mutant that also lacks Tyr-343 in combination with wild-type Flp will produce a catalytically inactive protein pair. This prediction could be directly tested in half-site reactions, since one could load the double mutant on a radioactively labeled half site and the wild-type protein on an unlabeled half site and then monitor

FIG. 2. Full-site substrates containing spacer mismatches. The sequences of the synthetic full sites used in the strand cleavage and strand transfer assays are shown. The <u>Flp</u>-binding elements are in boldface. Sequences flanking the <u>Flp</u> target site are represented by wavy lines. The positions of spacer mismatches (bubbles) are indicated. The experiments in which they were used are indicated by the corresponding figure numbers. S2n refers to a concatemer of S2 (8 to 10 monomeric units, on average). The spacer mismatches in S1 and S2 are such that strand swapping between the two substrates (following strand cleavage) would produce perfect complementarity.

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strand transfer only from the labeled substrate upon mixing of the prebound complexes (7). Thus, the background of wild-type

site is cleaved, the short spacer segment on the cleaved strand does not remain stably hydrogen bonded to its complementary sequence. Hence, it is effectively lost from the reaction center by diffusion. The 5(prm1)-hydroxyl group of the spacer on the noncleaved strand can then act as a phosphoryl acceptor to complete a half-site recombination event. Details of half-site reactions have been previously described (for example, see reference 22). Whereas two <u>Flp</u> monomers bound to a full site are restricted in their interactions by spacer connectivity, two half sites, each associated with a <u>Flp</u> monomer, are not subject to this constraint. They could potentially assume the configurations indicated. These correspond to variations of the trans interactions depicted in panel A.

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These results are consistent with the partial active-site model arrived at from half-site reactions (6). According to this model, a mutant pair can build an active site in which the RHR triad is contributed by <u>Flp(Y343F)</u> and Tyr-343 is contributed by the triad mutant. Therefore, strand cleavage becomes possible.

The nucleophile in the cleavage reaction by a pair of complementing <u>Flp</u> variants is Tyr-343: The partial-active-site model is based on the tacit assumption that strand cleavage is executed by the lone Tyr-343 present within a pair of the complementing protein monomers. The model would break down if, in the absence of Tyr-343, a substitute nucleophile in the form of a serine, threonine, cysteine, or another tyrosine could take up its function. We have ruled out the possibility of cis cleavage by a nucleophile other than Tyr-343 in complementation reactions with half sites (24). In the full-site context, activation of a surrogate nucleophile within Flp(Y343F) as a result of allosteric interactions among the protein monomers is not impossible. To test the surrogate nucleophile hypothesis, the assay was done with a bubbled full site labeled at the 5(prm1) end on both strands and a complementing pair of Flp variants made up of a normal-sized protein and a 30-kDa larger protein partner obtained as a fusion with GST. The protein-DNA adduct formed by <u>Flp</u> and the GST-<u>Flp</u> hybrid upon DNA cleavage can be distinguished by the difference in electrophoretic migration between them (lanes 2 and 3 in Fig. 4). Flp (Y343F) or GST-Flp(Y343F) did not yield the cleavage product, as expected (lanes 4 and 6 in Fig. 4). Flp(H305L) and GST-<u>Flp(H305L)</u> yielded low levels of the cleavage products with the expected mobilities (lanes 5 and 7 in Fig. 4). The low level of strand cleavage by these proteins was as predicted by the results shown in Fig. 3. However, in partnership with Flp (Y343F), they produced elevated levels of cleavage commensurate with catalytic complementation (lanes 8 and 9 in Fig. 4). When the complementing partners were GST-Flp(Y343F) and Flp(H305L), the size of the cleavage product matched that obtained from reactions with Flp (lane 8 in Fig. 4). When the reaction contained the reciprocal pair, Flp(Y343F) and GST-Flp(H305L), the

substrate (6, 17). However, attempts to obtain catalytic complementation between a triad mutant and Flp(Y343F) in full sites have not been successful. This is not surprising. In a recombination complex containing two monomers of each mutant oriented appropriately, a Holliday junction may be formed. Since the junction cannot be resolved into recombinants, the exchange reaction is reversed to restore the parental configuration. Demonstration of complementation therefore required the use of a suicide substrate in which the reaction intermediates could be readily trapped. We discovered that mismatches at certain positions within the strand exchange (spacer) region of a full site can strongly inhibit the strand-joining step of recombination, thus effectively transforming the sites harboring such mismatches into suicide substrates (unpublished data). For example, the substrate shown in Fig. 3 contains two adjacent mismatches each (bubbles) neighboring the cleavage points at the left and right ends of the spacer (Fig. 2). This substrate was cleaved efficiently by wild-type Flp. However, since strand joining was markedly slowed down (unpublished results), the cleavage product accumulated (lane 2 in Fig. 3). As expected, no cleavage was obtained with <u>Flp(Y343F)</u> (lane 3 in Fig. 3). <u>Flp</u> variants in which either of the two arginine residues from the RHR triad (Arg-191 and Arg-308) were changed failed to produce the cleavage product (lanes 4 and 8 in Fig. 3). It is known that Flp variants of the triad histidine can yield cleavage in a full site but are severely diminished in the ability to reseal strands (19). However, in a full site with the double bubble, cleavage by the histidine variants was significantly lowered relative to that obtained with wild-type Flp (compare lanes 6 and 2 in Fig. 3). It is possible that the absence of His-305, combined with the mismatched spacer configuration, perturbs the normal protein interactions that lead to catalysis. The histidine variants are also known to test as cleavage incompetent when provided with half-site substrates (23). When a triad arginine variant of Flp was mixed with Flp(Y343F), they complemented each other, as evidenced by the cleavage detected within the bubbled full site (lanes 5 and 9 in Fig. 3). Complementation was obtained when Flp (Y343F) was paired with the His-305 variant as well. Whereas cleavage with the His-305 variant alone was weak (lane 6 in Fig. the complementing pair yielded much higher levels of cleavage (lane 7 in Fig. 3).

FIG. 1. Full-site and half-site substrates for <u>Flp</u> site-specific recombination. (A) Each full site contains two invertedly oriented <u>Flp</u>-binding elements (parallel arrows) bordering the strand exchange region (spacer). There is a one-to-one association between a binding element and a <u>Flp</u> monomer. Conceptually, a full site can be split into a left half site (L) and a right half site (R). The phosphodiesters involved in recombination between two full sites are indicated (p). The placement of a <u>Flp</u> monomer with respect to these phosphodiesters can be described as cis (a), trans horizontal (b), trans vertical (c), or trans diagonal (d). (B) A half site contains one <u>Flp</u>-binding element and one scissile phosphodiester. When the

mixture containing 250 mM Tris-HCl (pH 7.8), 4% sodium dodecyl sulfate, 40% glycerol, and 300 mM (beta)-mercaptoethanol. Suitable aliquots were heated at 95 deg C for 4 min and fractionated by electrophoresis in 8% polyacrylamide gels (12). The gels were rinsed in distilled water with gentle shaking, dried, and subjected to autoradiography.

General methods:

Restriction enzyme digestions, isolation of plasmid DNA, and other miscellaneous procedures were done as described by Maniatis et al. (14).

RESULTS

The normal <u>Flp</u> reaction uses two double-stranded DNA substrates, each containing a copy of the Flp recombination target sequence (Fig. 1A). These are referred to as full-site substrates. A recombination event between two full sites requires the cooperative action of four Flp monomers and involves the breakage and reformation of four phosphodiester bonds within DNA (two breakage-union steps within each substrate partner). The disposition of a target-bound Flp monomer with respect to the four scissile phosphodiester bonds can be described as cis, trans horizontal, trans vertical, or trans diagonal. Conceptually, a full site can be split into two half sites, a left half site and a right half site. Half-site substrates (Fig. 1B), originally designed for the (lambda) Int reaction (15) and subsequently adapted for the Flp reaction (2, 21, 22), have simplified the mechanistic analysis of site-specific recombination. A half site contains one Flp-binding element, one scissile phosphodiester, and one 5(prm1)-hydroxyl group that can act as a phosphoryl acceptor. Hence, it is capable of undergoing one strand cleavage and one strand-joining reaction, precisely half of the chemistry that a full site undergoes during a normal recombination event. However, while interactions between two Flp monomers within a full site are constrained by the continuous DNA segment between them (the strand exchange region or the spacer), half sites are not subject to such constraints. Hence, two half sites could potentially interact with each other in a variety of modes that may not be accessible to two full sites (Fig. 1B). A legitimate concern, then, is that direct extrapolations from half-site to full-site reactions may not always be valid. To overcome this impediment, the analyses described here were done with appropriately modified full-site substrates (Fig. 2).

Pairwise complementation between $\underline{Flp}(Y343F)$ and the RHR triad variants of \underline{Flp} during strand cleavage in full sites: It is known that a \underline{Flp} variant altered at one or more of the RHR triad positions in combination with a second variant

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lacking the active-site nucleophile, <u>Flp(Y343F)</u>, can mediate a strand cleavage and a strand joining event within a half-site

heated to 65 deg C for 10 min, and cooled slowly to room temperature. The relevant features of these sites are described in Results and displayed in the figures. The complete sequences of the substrates are available upon request.

The 3(prm1) end of a deoxyoligonucleotide was labeled with (alpha)-(sup32)P-labeled cordycepin phosphate. Labeling at the 5(prm1) end was done by the T4 polynucleotide kinase reaction by using [(gamma)-(sup32)P]ATP as the phosphoryl donor. For some experiments, the 5(prm1) ends were phosphorylated with unlabeled ATP. The unreacted cordycepin phosphate or ATP was removed by spin dialysis on a G-25 column. Hybridization to the partner oligodeoxynucleotide was done in TE.

Strand cleavage assays:

Strand cleavage reactions were done under standard recombination conditions (6). Normally, 0.05 pmol of the 3(prm1) end-labeled substrate was reacted with approximately 0.5 pmol of Flp or a Flp variant (roughly 5 pmol of <u>Flp</u> per pmol of the binding element) in 30 (mu)l of the reaction mixture. Incubations were done at 30 deg C for 30 min. Reactions were stopped by immersing samples in a boiling water bath for 5 min. After addition of sodium dodecyl sulfate (final concentration, 0.1%) and proteinase K treatment (100 (mu)g per sample for 1 h at 37 deg C), samples were phenol-chloroform extracted and DNA was precipitated with ethanol. The DNA pellet was recovered by centrifugation, washed twice with 80% ethanol, and dried in vacuo. Strands were denatured in 95% formamide at 95 deg C, and samples were fractionated by electrophoresis in 10% denaturing polyacrylamide gels (acrylamide-bisacrylamide ratio, 19:1). Cleavage products were identified following autoradiography.

Strand transfer assays:

The synthetic full sites (approximately 45 to 50 bp long, carrying EcoRI and HindIII overhangs at the ends) were poor substrates in strand transfer. To increase the efficiency of the reaction, assays were done with the monomeric form of a radioactively labeled full site and the concatemeric form of the unlabeled full-site partner. The concatemer was prepared as follows. The full site phosphorylated at the 5(prm1) end on both strands was ligated at room temperature for 3 h under conditions that gave concatemers containing an average of 8 to 10 U of the monomer. The strand transfer reactions were done with the normal protocols described previously (6). The ratio of the labeled substrate to the monomeric equivalent of the unlabeled substrate was approximately 1:5. In these assays, approximately 6 to 8 pmol of <u>Flp</u> per pmol of the <u>Flp</u>-binding element was present in a reaction volume of 30 (mu)1. The samples were processed and fractionated as described for the strand cleavage assay.

Assay for formation of DNA-protein covalent adducts: Reactions were carried out under strand transfer conditions with a substrate labeled at the 5(prm1) ends on both strands. Reactions were quenched by addition of an equal volume of a stop

The catalytic strategies displayed by <u>Flp</u> and their mechanistic implications in recombination suggest that they may be universal to the Int family. One set of experiments with (lambda) Int using suicide attL substrates supports this notion. Catalytic complementation in pairwise combinations of the RHR triad mutants of Int with the active-site tyrosine mutant has been demonstrated (10). This result is strongly suggestive of trans DNA cleavage by Int. However, other results obtained by using suicide attB substrates and synthetic Holliday junctions are more parsimoniously explained in terms of cis DNA cleavage by Int (16).

The mechanistic dilemma posed by the Int results raises fundamental issues regarding the mechanism of Int family

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site-specific recombination. First, is the apparent cis-trans duality a basic feature of the reaction? Second, are there multiple modes of active-site assembly within this family? Finally, is the half-site reaction mechanistically distinct from the full-site reaction? We have devised an experimental design in which full sites carrying mismatches in the spacer region serve as substrates in complementation tests with step arrest Flp mutants. Our results fully support the shared active-site paradigm during full-site recombination. Furthermore, the mode of DNA cleavage is trans. We have found no evidence of cis-trans duality in Flp recombination.

MATERIALS AND METHODS

Purification of Flp:
Wild-type Flp and Flp variants were partially purified essentially as described by Prasad et al. (20). Strand cleavage and strand transfer assays were carried out with these preparations. Some reactions were done with 90 to 95% pure proteins obtained by an affinity purification protocol (18). Assays with affinity-pure proteins yielded the same results as those done with the less pure proteins. Fusion proteins composed of Flp (or a Flp variant) and glutathione S-transferase (GST) were purified in accordance with the procedure detailed by Yang and Jayaram (24). Protein concentrations were estimated by comparing densitometric scans of gel-fractionated aliquots stained with Coomassie brilliant blue to similar scans done with bovine serum albumin as the standard. These estimates were relatively crude and were only accurate within a factor of 2 or

Synthetic recombination sites:
Oligodeoxynucleotides for construction of full sites were
synthesized in an Applied Biosystems 380A DNA synthesizer by
using phosphoramidite chemistry (4). Normally, 10 to 20 pmol of
each of the two appropriate oligodeoxynucleotide pairs was mixed
in TE (10 mM Tris-HCl [pH 7.8] at 23 deg C, 1 mM EDTA [pH 8.0]),

intermediate which, following branch migration, is resolved into recombinants by the second pair of cleavage-joining reactions. The Int family recombinases use an active-site tyrosine as the nucleophile to attack the scissile phosphodiester during the strand breakage step. In Flp, this tyrosine residue is Tyr-343 (9). The active-site tyrosine is one of the invariant tetrad residues of the Int family (1, 3). The other three invariant residues are two arginines and a histidine (the RHR triad; Arg-191, His-305, and Arg-308 in Flp). The strand cleavage reaction results in covalent attachment of the recombinase to the 3(prm1) phosphate of DNA and exposure of a 5(prm1)-hydroxyl group at the nick. Strand joining in the recombinant mode is then effected via nucleophilic attack, by the 5(prm1)-hydroxyl group from the nicked strand of one DNA substrate, on the 3(prm1)-phosphotyrosyl bond formed within the partner substrate.

The Int family recombinases exist in solution as monomers and bind to DNA as monomers. Four recombinase monomers must act cooperatively to accomplish one round of recombination. Two concerted break exchanges must be made at one end of the strand exchange region (spacer) to form the Holliday junction. The process then needs to be repeated at the other end of the spacer to resolve the junction into mature recombinants. How does an Int family recombinase coordinate the breakage-joining events within the two DNA substrates taking part in recombination? Does the recombinase have a built-in mechanism by which it avoids abortive partial reactions within an incompletely assembled reaction complex?

The active-site configuration of two Int family members, Flp and the Zygosaccharomyces rouxii recombinase R, inferred from recombination reactions containing half-site substrates and step arrest mutants of the recombinases suggests potential solutions to the problems addressed above (6, 7, 13, 17, 24). A monomer of Flp or R harbors a partial active site; a complete active site is assembled by contribution of residues from more than one recombinase monomer. In the shared active site, three of the invariant Int family residues, the RHR triad (Arg-191, His-305, and Arg-308 in Flp; Arg-207, His-317, and Arg-320 in R), are derived from one monomer; the active-site tyrosine (Tyr-343 in Flp and Tyr-358 in R) is provided by a second monomer (6, 17). Assembly of a functional active site from partial active sites neatly accommodates the observation that in reactions with half sites, an Flp or an R monomer does not cleave the substrate to which it is bound but rather cleaves the substrate bound by a second recombinase monomer (trans DNA cleavage; 6). The partial active site, together with the trans mode of DNA cleavage, suggests possible mechanisms for postponing the chemistry of recombination until the complex is fully organized, for simultaneously assembling two active sites for coordinated strand cleavages, and for coupling the cleavage reaction with the conformational switch required for strand joining between partner substrates.

Title: Active-Site Assembly and Mode of DNA Cleavage by Flp

Recombinase during Full-Site Recombination

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Abstract: A combination of half-site substrates and step

arrest mutants of Flp, a site-specific recombinase of the integrase family, had earlier revealed the following features of the half-site recombination reaction. (i) The <u>Flp</u> active site is assembled by sharing of catalytic residues from at least two monomers of the protein. (ii) A Flp monomer does not cleave the half site to which it is bound (DNA cleavage in cis); rather, it cleaves a half site bound by a second Flp monomer (DNA cleavage in trans). For the (lambda) integrase (Int protein), the prototype member of the Int family, catalytic complementation between two active-site mutants has been observed in reactions with a suicide attL substrate. By analogy with <a>Flp, this observation is strongly suggestive of a shared active site and of trans DNA cleavage. However, reactions with linear suicide attB substrates and synthetic Holliday junctions are more compatible with cis than with trans DNA cleavage. These Int results either argue against a common mode of active-site assembly within the Int family or challenge the validity of Flp half sites as mimics of the normal full-site substrates. We devised a strategy to assay catalytic complementation between Flp monomers in full sites. We found that the full-site reaction follows the shared active-site paradigm and the trans mode of

DNA cleavage. These results suggest that within the Int family, a unitary chemical mechanism of

recombination is achieved by more than one mode of

physical interaction among the recombinase monomers.

Text:

The <u>Flp</u> protein of Saccharomyces cerevisiae is a conservative, site-specific DNA recombinase that belongs to the Int ((lambda) integrase) family of recombinases (1, 3). Members of this family execute recombination in two sequential steps. The first pair of strand cleavage-joining reactions produces a Holliday

172190

Definition Yeast (S.cerevisiae) 2 micron circle plasmid, complete genome

GenBank Name: YSCPLASM, Accession: J01347

NCBI Seq ID: 172190

Organism Saccharomyces cerevisiae

Comment [8] sites; mRNA CAP sites and poly-adenylation sites. [9] sites; FLP binding.

[7] sites; FLP cleavage.

[11] sites; FLP-mediated recombination crossover site. Draft entry and clean copy sequence for [5] kindly provided by J.Senecoff, 24-JAN-1986.

Yeast 2 micron plasmid contains two 599 bp inverted repeats separated by a large unique (UL) and a small unique (US) region. During recombination the UL and US regions invert producing two sequence forms that differ in the orientation of one unique region relative to the other. The A form is presented below. FLP is the only 2-micron circleencoded protein needed for specific site recombination between the IRs of 2-micron circle. The minimal size of the recombination site required for efficient FLP recombinase-catalyzed recombination in vitro is no more than 28 bp, which includes parts of two 13 bp inverted repeats (positions 690-702 and 711-723) and all of an 8 bp spacer (703-710) [5]. The FLP recombinase cleaves the DNA at the boundaries of the spacer and becomes covalently linked to the spacer DNA [5],[9]. The efficiency of the recombination is reduced if the spacer in a recombinant site is increased or decreased by 1 bp, while the spacer in the second site is unaltered [5]. Recombination between two sites with identical 1-base pair additions or deletions is relatively unaffected, suggesting that pairing of sequences in the spacer regions is important in FLP-promoted recombination events [5]. The sequence asymmetry utilized by the recombinase to determine the orientation of the site is located uniquely within the spacer region. Another 13 bp direct repeat, is found at positions 676-688 [5]. FLP-mediated recombination involving two FLP sites that are inverted with respect to each other results in inversion of the DNA sequences between the sites [4]. If the participating recombination sites are in direct orientation, FLP promotes only the excision of the intervening DNA sequences [4]. The Rep 1 and Rep proteins are involved plasmid partitioning and protein stability.

A start codon in phase with the Rep1 coding region is located at positions 1966-1964. Two CAP sites for Rep1 mRNA are located beyond the 'atg' codon (position 2008) at positions 2004 and 2005. Complete source information:

Yeast (S. cerevisiae, strain A364A D5) DNA, clones pJDB71 [1], p82-6B [2], CV20 [3], pMMD2 [4], pGP20 [5], pJFS166 [10].

Updated

Jul 31, 1992

Coding region 172190: 5570..6318 172190: 1..523

Coding region 172190: c2008..887

Coding region 172190: 2271..2816

Coding region 172190: c5198..4308

Sequence 6318 nt, circular ds genomic

1 gaattetgaa ceagteetaa aacgagtaaa taggacegge aattetteaa 5 gcaataaaca ggaataccaa ttattaaaag ataacttagt cagatcgtac 101 aataaagett tgaagaaaaa tgegeettat teaatetttg etataaaaaa 151 tggcccaaaa tctcacattg gaagacattt gatgacctca tttctttcaa 201 tgaagggcct aacggagttg actaatgttg tgggaaattg gagcgataag 251 cgtgcttctg ccgtggccag gacaacgtat actcatcaga taacagcaat 301 acctgatcac tacttogcac tagtttctcg gtactatgca tatgatccaa 351 tatcaaagga aatgatagca ttgaaggatg agactaatcc aattgaggag 401 tggcagcata tagaacagct aaagggtagt gctgaaggaa gcatacgata 451 ccccgcatgg aatgggataa tatcacagga ggtactagac tacctttcat 501 cctacataaa tagacgcata taagtacgca tttaagcata aacacgcact 551 atgccgttct tctcatgtat atatatac aggcaacacg cagatatagg 601 tgcgacgtga acagtgagct gtatgtgcgc agctcgcgtt gcattttcgg 651 aagcgctcgt tttcggaaac gctttgaagt tcctattccg aagttcctat 701 tetetagaaa gtataggaac tteagagege ttttgaaaac caaaageget 751 ctgaagacgc actttcaaaa aaccaaaaac gcaccggact gtaacgagct 801 actaaaatat tgcgaatacc gcttccacaa acattgctca aaagtatctc 851 tttgctatat atctctgtgc tatatcccta tataacctac ccatccacct 901 ttcgctcctt gaacttgcat ctaaactcga cctctacatc aacaggcttc 951 caatgetett caaattttac tgtcaagtag acceatacgg ctgtaatatg 1001 ctgctcttca taatgtaagc ttatctttat cgaatcgtgt gaaaaactac 1051 taccgcgata aacctttacg gttccctgag attgaattag ttcctttagt 1101 atatgataca agacactttt gaactttgta cgacgaattt tgaggttcgc 1151 catcetetgg ctatttecaa ttateetgte ggetattate teegeeteag 1201 tttgatcttc cgcttcagac tgccattttt cacataatga atctatttca 1251 ccccacaatc cttcatccgc ctccgcatct tgttccgtta aactattgac 1301 ttcatgttgt acattgttta gttcacgaga agggtcctct tcaggcggta 1351 getectgate tectatatga cetttateet gttetettte cacaaactta 1401 gaaatgtatt catgaattat ggagcaccta ataacattct tcaaggcgga 1451 gaagtttggg ccagatgccc aatatgcttg acatgaaaac gtgagaatga 1501 atttagtatt attgtgatat tctgaggcaa ttttattata atctcgaaga 1551 taagagaaga atgcagtgac ctttgtattg acaaatggag attccatgta 1601 totaaaaaat acgcotttag goottotgat accotttoco otgoggttta 1651 gegtgeettt tacattaata tetaaaceet eteegatggt ggeetttaac

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1851 aatgcaaatg ctaacgtttt gtatttctta taattgtcag gaactggaaa
1901 agteceett gtegtetega ttacacacet actttcateg tacaccatag
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2051 gcgctgtaaa aatctatctg ttacagaagg ttttcgcggt ttttataaac
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2201 tgattaactt cgagaaggga ttaaggctaa tttcactagt atgtttcaaa
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3751 aaaggtggat gggtaggtta tatagggata tagcacagag atatatagca

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4351 gttgctactc tcctttttt cgtgggaacc gctttagggc cctcagtgat
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5051 agagtagete atcagactta egtttactet etatateaat atetacatea
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5301 gatagtaccg caaaacgaac ctgcgggccg tctaaaaatt aaggaaaagc
5351 agcaaaggtg catttttaaa atatgaaatg aagataccgc agtaccaatt
5401 attttcgcag tacaaataat gcgcggccgg tgcatttttc gaaagaacgc
5451 gagacaaaca ggacaattaa agttagtttt tcgagttagc gtgtttgaat
5501 actgcaagat acaagataaa tagagtagtt gaaactagat atcaattgca
5551 cacaagateg gegetaagea tgecacaatt tggtatatta tgtaaaacac
5601 cacctaaggt gettgttegt eagtttgtgg aaaggtttga aagacettea
5651 ggtgagaaaa tagcattatg tgctgctgaa ctaacctatt tatgttggat
5701 gattacacat aacggaacag caatcaagag agccacattc atgagctata
5751 atactatcat aagcaattcg ctgagtttcg atattgtcaa taaatcactc
5801 cagtttaaat acaagacgca aaaagcaaca attctggaag cctcattaaa
5851 gaaattgatt cctgcttggg aatttacaat tattccttac tatggacaaa
5901 aacatcaatc tgatatcact gatattgtaa gtagtttgca attacagttc
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- 5951 gaatcatcgg aagaagcaga taagggaaat agccacagta aaaaaatgct
 6001 taaagcactt ctaagtgagg gtgaaagcat ctgggagatc actgagaaaa
 6051 tactaaattc gtttgagtat acttcgagat ttacaaaaac aaaaacttta
 6101 taccaattcc tcttcctagc tactttcatc aattgtggaa gattcagcga
 6151 tattaagaac gttgatccga aatcatttaa attagtccaa aataagtatc
 6201 tgggagtaat aatccagtgt ttagtgacag agacaaagac aagcgttagt
- 6301 tttggatgaa tttttgag

486,489 PLEASE ENTER HOST PORT ID:x LOGINID: d184csl PASSWORD: TERMINAL (ENTER 1, 2, 3, 4, OR ?):2e P0001 U.S. Patent & Trademark Office 06 JUN 92 14:03:30 => set pagelength scroll SET COMMAND COMPLETED => s flp(5a)recombinas? 151 FLP 6 RECOMBINAS? 1 FLP(5A)RECOMBINAS? Ll => d 1. 4,997,757, Mar. 5, 1991, Process for detecting potential carcinogens; Robert H. Schiestl, 435/172.1, 6, 29, 172.3; 935/76, 78, 79, 84 [IMAGE AVAILABLE] => Alt-2 FOR HELP| VT102 | FDX | 2400 N81 | LOG CLOSED | PRINT OFF | ON-LINE d his (FILE 'USPAT' ENTERED AT 14:03:27 ON 06 JUN 92) SET PAGELENGTH SCROLL 1 S FLP(5A) RECOMBINAS? L1 L2 1 S L1 AND MAMMAL? FILE 'JPOABS' ENTERED AT 14:06:27 ON 06 JUN 92 L3 0 S L1 FILE 'USPAT' ENTERED AT 14:06:43 ON 06 JUN 92 => d 'L3' HAS NO ANSWERS O SEA FLP(5A)RECOMBINAS? $=> d_{11}$ 1. 4,997,757, Mar. 5, 1991, Process for detecting potential carcinogens; Robert H. Schiestl, 435/172.1, 6, 29, 172.3; 935/76, 78, 79, 84 [IMAGE **AVAILABLE** edecqt ∵iil <* FILE ' 'POABS' ENTERED AT 14:07:11 ON 06 JUN 92 JAPANESE PATENT ABSTRACTS * CURRENTLY, DATA IS LOADED THROUGH THE ABSTRACT PUBLICATION * * DATE OF AUGUST 30, 1991. * THE LATEST GROUPS RECEIVED ARE: C0862 E1105, M1150 & P1245. *

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21 FLP

0 RECOMBINAS?

0 FLP(5A)RECOMBINAS?

(Item 1 from file: 155) 2/3/1 08128396 92266396 cleavage in trans by the active site tyrosine during Flp recombination: switching protein partners before exchanging strands. Chen JW; Lee J; Jayaram M Department of Microbiology, University of Texas, Austin 78712. Cell (UNITED STATES) May 15 1992, 69 (4) p647-58, ISSN 0092-8674 Journal Code: CQ4 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/2 (Item 2 from file: 155) 08080444 92218444 Reactions between Malf- and full-FLP recombination target sites. A model system for analyzing early steps in FLP protein-mediated site-specific recombination. Qian XH; Inmay RB; Cox MM Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706. J Biol Chem (UNITED STATES) 0021-9258 Journal Code: HIV Apr 15 1992, 267 (11) p7794-805, Contract/Grant No.: GM-32335; GM-14711 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/3 (Item 3 from file: 155) 07913378 92051378/ FLP-mediated regembination in the vector mosquito, Aedes aegypti. Morris AC; Schaub TL; James AA Department of Molecular Biology & Biochemistry, University of California, Irvine 92717/. Nucleic / Acids Res (ENGLAND) Nov 11 1991, 19 (21) p5895-900, ISSN 0305-1048 Journal Code: 08L Languages: ENGLISH Dogument type: JOURNAL ARTICLE 2/3/4 (Item 4 from fi∕îe: 155) 07823652 91342652 Synapsis, strand scission, and strand exchange induced by the FLP recombinase: analysis with half-FRT sites. Amin A; Roca H; Luetke K; Sadowski PD Department of Medical Genetics, University of Toronto, Ontario, Canada. Mol Cell Biol Sep 1991, 11 (9) p4497-508, ISSN 0270-7306 Journal Code: NGY Languages: ENGLISH Document type: JOURNAL ARTICLE (Item 5 from file: 155) 07777737 91296737 Domain of a yeast site-specific recombinase (Flp) that recognizes its target site.

Chen JW; Evans BR; Yang SH; Teplow DB; Jayaram M
Department of Microbiology, University of Texas, Austin 78712.
Proc Natl Acad Sci U S A Jul 15 1991, 88 (14) p5944-8, ISSN 0027-8424
Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/6 (Item 6 from file: 155)

07731454 91250454

Identification of the DNA-binding domain of the FLP recombinase.

Pan H; Clary D; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Biol Chem Jun 15 1991, 266 (17) p11347-54, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/7 (Item 7 from file: 155)

07687992 91206992

Integration specificity of retrotransposons and retroviruses.

Sandmeyer SB; Hansen LJ; Chalker DL

Department of Microbiology and Molecular Genetics, College of Medicine, University of California, Irvine 92717.

Annu Rev Genet 1990, 24 p491-518, ISSN 0066-4197 Journal Code: 6DF Contract/Grant No.: GM33281

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC

2/3/8 (Item 8 from file: 155)

07668658 91187658

A bacterial model system for chromosomal targeting.

Huang LC; Wood EA; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Nucleic Acids Res Feb 11 1991, 19 (3) p443-8, ISSN 0305-1048 Journal Code: O&L

Contract/Grant No.: GM37835

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/9 (Item 9 from file: 155)

07645850 91164850

Recombinase-mediated gene activation and site-specific integration in mammalian cells.

O'Gorman S; Fox DT; Wahl GM

Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

Science Mar 15 1991, 251 (4999) p1351-5, ISSN 0036-8075

Journal Code: UJ7

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/10 (Item 10 from file: 155)

07643634 91162634

Tyr60 variants of Flp recombinase generate conformationally alteremente in DNA complexes. Differential activity in full-site and half-site recombinations.

Chen JW; Evans BR; Zheng L; Jayaram M

Department of Microbiology, University of Texas at Austin, Austin 78712.

J Mol Biol Mar 5 1991, 218 (1) p107-18, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/11 (Item 11 from file: 155)

07554393 91073393

 FLP protein of 2 mu circle plasmid of yeast induces multiple bends in the FLP recognition target site.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1990, 216 (2) p289-98, ISSN 0022-2836

Journal Code: JGV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/12 (Item 12 from file: 155)

07553382 91072382

Protein-based asymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination.

Qian XH; Inman RB; Cox MM

Program in Cell and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706.

J Biol Chem Dec 15 1990, 265 (35) p21779-88, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM 37835; GM 14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/13 (Item 13 from file: 155)

07490349 91009349

Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination [published erratum appears in J Biol Chem 1991 Apr 15;266(11):7312]

Evans BR; Chen JW; Parsons RL; Bauer TK; Teplow DB; Jayaram M Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Oct 25 1990, 265 (30) p18504-10, ISSN 0021-9258 Journal Code: HIV

outhar code: 1110

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/14 (Item 14 from file: 155)

07410836 90317836

Synaptic intermediates promoted by the FLP recombinase.

Amin AA; Beatty LG; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Jul 5 1990, 214 (1) p55-72, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/15 (Item 15 from file: 155)

07263960 90170960

Functional analysis of Arg-308 mutants of Flp recombinase. Possible role of Arg-308 in coupling substrate binding to catalysis.

Parsons RL: Evans BR: Zheng L: Jayaram M

Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Mar 15 1990, 265 (8) p4527-33, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/16 (Item 16 from file: 155)

07229522 90136522

Use of site-specific recombination to regenerate selectable markers.

Cregg JM; Madden KR

Salk Institute Biotechnology/Industrial Associates, Inc., La Jolla, CA 92037.

Mol Gen Genet Oct 1989, 219 (1-2) p320-3, ISSN 0026-8925

Journal Code: NGP Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/17 (Item 17 from file: 155)

07190832 90097832

Characterization of Holliday structures in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Inman RB; Cox MM

Program in Cellular and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Jan 1990, 10 (1) p235-42, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/18 (Item 18 from file: 155)

07123422 90030422

The FLP recombinase of yeast catalyzes site-specific recombination in the Drosophila genome.

Golic KG; Lindquist S

Howard Hughes Medical Institute, Department of Molecular Genetics and Cell Biology, University of Chicago, Illinois 60637.

Cell Nov 3 1989, 59 (3) p499-509, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM 25874

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/19 (Item 19 from file: 155)

07011744 89313744

Synthesis of an enzymatically active FLP recombinase in vitro: search for a DNA-binding domain.

Amin AA; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

Mol Cell Biol May 1989, 9 (5) p1987-95, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/20 (Item 20 from file: 155)

07002130 89304130

FLP-FRT mediated intrachromosomal recombination on a tandemly duplicated YEp integrant at the ILV2 locus of chromosome XIII in Saccharomyces cerevisiae.

Rank GH; Arndt GM; Xiao W

Department of Biology, University of Saskatchewan, Saskatoon, Canada.

Curr Genet Feb 1989, 15 (2) p107-12, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/21 (Item 21 from file: 155)

06876684 89178684

FLP recombinase of the 2 microns circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Feb 20 1989, 205 (4) p647-58, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/22 (Item 22 from file: 155)

06825220 89127220

Holliday intermediates and reaction by-products in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Huang LC; Umlauf SW; Cox MM; Inman RB

Department of Biochemistry, College of Agriculture and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Sep 1988, 8 (9) p3784-96, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/23 (Item 23 from file: 155)

06823587 89125587

The mechanism of loading of the FLP recombinase onto its DNA target sequence.

Beatty LG; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1988, 204 (2) p283-94, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/24 (Item 24 from file: 155)

06794920 89096920

Step-arrest mutants of FLP recombinase: implications for the catalytic mechanism of DNA recombination.

Parsons RL; Prasad PV; Harshey RM; Jayaram M

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

Mol Cell Biol Aug 1988, 8 (8) p3303-10, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/25 (Item 25 from file: 155)

06761437 89063437

High frequency FLP-independent homologous DNA recombination of 2 mu plasmid in the yeast Saccharomyces cerevisiae.

Bruschi CV: Howe GA

Department of Microbiology and Immunology, School of Medicine, East Carolina University, Greenville, NC 27858-4354.

Curr Genet Sep 1988, 14 (3) p191-9, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/26 (Item 26 from file: 155)

06740094 89042094

Holliday junctions in FLP recombination: resolution by step-arrest mutants of FLP protein.

Jayaram M; Crain KL; Parsons RL; Harshey RM

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, CA 92037.

Proc Natl Acad Sci U S A Nov 1988, 85 (21) p7902-6, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/27 (Item 27 from file: 155)

06703077 89005077

The functional significance of DNA sequence structure in a site-specific genetic recombination reaction.

Umlauf SW; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

EMBO J Jun 1988, 7 (6) p1845-52, ISSN 0261-4189 Journal Code: EMB Contract/Grant No.: GM37835; AI00599; GM07215

Languages: ENGLISH

Document type: JOURNAL ARTICLE,

2/3/28 (Item 28 from file: 155)

06687975 88332975

DNA recognition by the FLP recombinase of the yeast 2 mu plasmid. A mutational analysis of the FLP binding site.

Senecoff JF; Rossmeissl PJ; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

J Mol Biol May 20 1988, 201 (2) p405-21, ISSN 0022-2836

Journal Code: J6V

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/29 (Item 29 from file: 155)

06643050 88288050

Nucleotide sequencing and expression of the fadL gene involved in long-chain fatty acid transport in Escherichia coli.

Said B; Ghosn CR; Vu L; Nunn WD

Department of Molecular Biology and Biochemistry, University of California, Irvine 92717.

Mol Microbiol May 1988, 2 (3) p363-70, ISSN 0950-382X

Journal Code: MOM

Contract/Grant No.: GM 22466-11

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/30 (Item 30 from file: 155)

06618001 88263001

FLP recombinase is an enzyme.

Gates CA; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Proc Natl Acad Sci U S A Jul 1988, 85 (13) p4628-32, ISSN 0027-8424 Journal Code: PV3

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/31 (Item 31 from file: 155)

06567126 88212126

Mutations that improve the binding of yeast FLP recombinase to its substrate.

Lebreton B; Prasad FV; Jayaram M; Youderian P

Department of Biological Sciences, University of Southern California, Los Angeles 90089-1481.

Genetics Mar 1988, 118 (3) p393-400, ISSN 0016-6731 Journal Code: FNH

Contract/Grant No.: GM34982; GM35654

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/32 (Item 32 from file: 155)

06521666 88166666

Antagonistic controls regulate copy number of the yeast 2 mu plasmid. Murray JA; Scarpa M; Rossi N; Cesareni G

EMBL, Heidelberg, FRG.

EMBO J Dec 20 1987, 6 (13) p4205-12, ISSN 0261-4189 Journal Code: EMB

Languages: ENGLISH

2/3/33 (Item 33 from file: 155)

06506025 88151025

Autoregulation of 2 micron circle gene expression provides a model for maintenance of stable plasmid copy levels.

Som T; Armstrong KA; Volkert FC; Broach JR

Department of Molecular Biology, Princeton University, New Jersey 08544.

Cell Jan 15 1988, 52 (1) p27-37, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/34 (Item 34 from file: 155)

06342913 87316913

Purification of the FLP site-specific recombinase by affinity chromatography and re-examination of basic properties of the system.

Meyer-Leon L; Gates CA; Attwood JM; Wood EA; Cox MM

Nucleic Acids Res Aug 25 1987, 15 (16) p6469-88, ISSN 0305-1048

Journal Code: O&L

Contract/Grant No.: GM32335; GM37835; AI00599; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/35 (Item 35 from file: 155)

06280212 87254212

Isolation of intermediates in the binding of the FLP recombinase of the yeast plasmid 2-micron circle to its target sequence.

Andrews BJ; Beatty LG; Sadowski PD

J Mol Biol Jan 20 1987, 193 (2) p345-58, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/36 (Item 36 from file: 155)

06274060 87248060

Rapid localization and characterization of random mutations within the 2 micron circle site-specific recombinase: a general strategy for analysis of protein function [published erratum appears in Gene 1987;57(1):149]

Govind NS; Jayaram M

Gene 1987, 51 (1) p31-41, ISSN 0378-1119 Journal Code: FOP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/37 (Item 37 from file: 155)

06210407 87184407

Site-specific recombination of the yeast plasmid two-micron circle: intermediates in the binding process.

Andrews BJ; Beatty LG; Sadowski PD

Basic Life Sci 1986, 40 p407-24, ISSN 0090-5542 Journal Code: 9K0

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/38 (Item 38 from file: 155)

06210406 87184406

Site-specific recombination promoted in vitro by the FLF protein of the yeast two-micron plasmid.

Senecoff JF; Bruckner RC; Meyer-Leon L; Gates CA; Wood E; Umlauf SW; Attwood JM; Cox MM

Basic Life Sci 1986, 40 p397-405, ISSN 0090-5542 Journal Code: 9K0 Contract/Grant No.: GM32335; 5-T32 GM07215; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/39 (Item 39 from file: 155)

06210404 87184404

Survival strategies of the yeast plasmid two-micron circle.

Volkert FC; Wu LC; Fisher PA; Broach JR

Basic Life Sci 1986, 40 p375-96, ISSN 0090-5542 Journal Code: 9K0

Contract/Grant No.: GM34596; GM33132

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/40 (Item 40 from file: 155)

06201639 87175639

Mutations in the 2-microns circle site-specific recombinase that abolish recombination without affecting substrate recognition [published erratum appears in Proc Natl Acad Sci U S A 1988 Mar;85(5):1497]

Prasad PV; Young LJ; Jayaram M

Proc Natl Acad Sci U S A Apr 1987, 84 (8) p2189-93, ISSN 0027-8424 Journal Code: FV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/41 (Item 41 from file: 155)

06167165 87141165

Association of reciprocal exchange with gene conversion between the repeated segments of 2-micron circle.

Jayaram M

J Mol Biol Oct 5 1986, 191 (3) p341-54, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/42 (Item 42 from file: 155)

06115790 87089790

Substrate recognition by the 2 micron circle site-specific recombinase: effect of mutations within the symmetry elements of the minimal substrate.

Prasad FV; Horensky D; Young LJ; Jayaram M

Mol Cell Biol Dec 1986, 6 (12) p4329-34, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM 35654-01

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/43 (Item 43 from file: 155)

06115725 87089725

Mating type-like conversion promoted by the 2 micrograms circle

site-specific recombinase: implications for the double-strand-gap repair model.

Jayaram M

Mol Cell Biol Nov 1986, 6 (11) p3831-7, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/44 (Item 44 from file: 155)

06115667 87089667

Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 microns circle.

McLeod M; Craft S; Broach JR

Mol Cell Biol Oct 1986, 6 (10) p3357-67, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

' 2/3/45 (Item 45 from file: 155)

06090546 87064546

Interaction of the FLP recombinase of the Saccharomyces cerevisiae 2 micron plasmid with mutated target sequences.

Andrews BJ; McLeod M; Broach J; Sadowski PD

Mol Cell Biol Jul 1986, 6 (7) p2482-9, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/46 (Item 46 from file: 155)

06009798 86310798

The FLP recombinase of the Saccharomyces cerevisiae 2 microns plasmid attaches covalently to DNA via a phosphotyrosyl linkage.

Gronostajski RM; Sadowski PD

Mol Cell Biol Nov 1985, 5 (11) p3274-9, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JBURNAL ARTICLE

2/3/47 (Item 47 from file: 155)

06003314 86304314

Specific contacts between the FLP protein of the yeast 2-micron plasmid and its recombination site.

Bruckner RC; Cox MM

J Biol Chem Sep 5 1986, 261 (25) p11798-807, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/48 (Item 48 from file: 155)

05983659 86284659

Chromatin organization of the Saccharomyces cerevisiae 2 microns plasmid depends on plasmid-encoded products.

Veit BE; Fangman WL

627

Mol Cell Biol Sep 1985, 5 (9) p2190-6, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM18926

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/49 (Item 49 from file: 155)

05980709 86281709

FLP site-specific recombinase of yeast 2-micron plasmid. Topological features of the reaction.

Beatty LG; Babineau-Clary D; Hogrefe C; Sadowski PD

J Mol Biol Apr 20 1986, 188 (4) p529-44, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/50 (Item 50 from file: 155)

05971102 86272102

Site-specific recombination promotes plasmid amplification in yeast.

Volkert FC; Broach JR

Cell Aug 15 1986, 46 (4) p541-50, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM-34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/51 (Item 51 from file: 155)

05958059 86259059

The minimal duplex DNA sequence required for site-specific recombination promoted by the FLP protein of yeast in vitro.

Proteau G; Sidenberg D; Sadowski P

Nucleic Acids Res Jun 25 1986, 14 (12) p4787-802, ISSN 0305-1048

Journal Code: O&L Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/52 (Item 52 from file: 155)

05931585 86232585

Sequence organization of the circular plasmid pKD1 from the yeast Kluyveromyces drosophilarum.

Chen XJ; Saliola M; Falcone C; Bianchi MM; Fukuhara H

Nucleic Acids Res Jun 11 1986, 14 (11) p4471-81, ISSN 0305-1048

Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/53 (Item 53 from file: 155)

05923006 86224006

Directionality in FLP protein-promoted site-specific recombination is mediated by DNA-DNA pairing.

Senecoff JF; Cox MM

J Biol Chem Jun 5 1986, 261 (16) p7380-6, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/54 (Item 54 from file: 155)

05919123 86220123

The integrase family of site-specific recombinases: regional similarities and global diversity.

Argos P; Landy A; Abremski K; Egan JB; Haggard-Ljungquist E; Hoess RH; Kahn ML; Kalionis B; Narayana SV; Pierson LS 3d; et al

EMBO J Feb 1986, 5 (2) p433-40, ISSN 0261-4189 Journal Code: EMB

Contract/Grant No.: AI 13544

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/55 (Item 55 from file: 155)

05810590 86111590

Site-specific recombinases: changing partners and doing the twist. Sadowski ${\sf P}$

J Bacteriol Feb 1986, 165 (2) p341-7, ISSN 0021-9193 Journal Code: HH3

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW

2/3/56 (Item 56 from file: 155)

05741647 86042647

The FLP recombinase of the yeast 2-micron plasmid: characterization of its recombination site.

Senecoff JF; Bruckner RC; Cox MM

Proc Natl Acad Sci U S A Nov 1985, 82 (21) p7270-4, ISSN 0027-8424 Journal Code: PV3

Contract/Grant No.: GM32335

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/57 (Item 57 from file: 155)

05707309 86008309

The FLP protein of the 2-micron plasmid of yeast. Inter- and intramolecular reactions.

Gronostajski RM; Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12328-35, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/58 (Item 58 from file: 155)

05707308 86008308

 \cdot Determination of DNA sequences essential for FLP-mediated recombination by a novel method.

Gronostajski RM; Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12320-7, ISSN 0021-9258

Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/59 (Item 59 from file: 155)

05707307 86008307

The FLP protein of the 2-micron plasmid of yeast. Purification of the protein from Escherichia coli cells expressing the cloned FLP gene.

Babineau D; Vetter D; Andrews BJ; Gronostajski RM; Proteau GA; Beatty LG; Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12313-9, ISSN 0021-9258 Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/60 (Item 60 from file: 155)

05560933 85176933

The FLP recombinase of the 2 micron circle DNA of yeast: interaction with its target sequences.

Andrews BJ; Proteau GA; Beatty LG; Sadowski FD

Cell Apr 1985, 40 (4) p795-803, ISSN 0092-8674 Journal Code: CQ4

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/61 (Item 1 from file: 5) 8906509 BIOSIS Number: 42131509

AN ORDERED DISASSEMBLY OF COMPLEXES OF FLP RECOMBINASE AND FRT SITES FOLLOWING RECOMBINATION

WAITE L L; COX M M

DEP. BIOCHEM., UNIV. WISCONSIN, MADISON, WIS. 53706.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 67. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/62 (Item 2 from file: 5)

8906501 BIOSIS Number: 42131501

LIGATION ACTIVITY OF THE FLP RECOMBINASE

PAN G; SADOWSKI P D

DEP. MOLECULAR MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 65. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/63 (Item 3 from file: 5)

8906498 BIOSIS Number: 42131498

HALF-SITE RECOMBINATIONS MEDIATED BY FLP RECOMBINASE FROM SACCHAROMYCES-CEREVISIAE

SERRE M-C; LEI-ZHENG; JAYARAM M

DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78746.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 64. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/64 (Item 4 from file: 5) 8906492 BIOSIS Number: 42131492 FUNCTIONAL ANALYSES OF MUTANTS OF FLP AND R RECOMBINASE FROM YEAST CHEN J-W; LEE J; EVANS B; SERRE M-C; ARAKI H; OSHIMA Y; JAYARAM M DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL RIOCHEM SUPPL 0 (16 PART B). 1992. 62. CODEN: JCBSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/65 (Item 5 from file: 5) 8197568 BIOSIS Number: 91118568 TYROSINE-60 VARIANTS OF FLP RECOMBINASE GENERATE CONFORMATIONALLY ALTERED PROTEIN DNA COMPLEXES DIFFERENTIAL ACTIVITY IN FULL-SITE AND HALF RECOMBINATIONS CHEN J-W; EVANS R R; ZHENG L; JAYARAM M DEP. MICRBOIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712, USA. J MOL BIOL 218 (1). 1991. 107-118. CODEN: JMOBA Full Journal Title: Journal of Molecular Biology Language: ENGLISH 2/3/66 (Item 6 from file: 5) 7103760 BIOSIS Number: 88026505 FLP-FRT MEDIATED INTRACHROMOSOMAL RECOMBINATION ON A TANDEMLY DEPLICATED YE-P INTEGRANT AT THE ILV2 LOCUS OF CHROMOSOME XIII IN SACCHAROMYCES-CEREVISIAE RANK G H; ARNDT G M; XIAO W DEP. BIOL., UNIV. SASKATCHEWAN, SASKATOON, SASKATCHEWAN, CANADA S7N 0W0. CURR GENET 15 (2). 1989. 107-112. CODEN: CUGED Full Journal Title: Current Genetics Language: ENGLISH 2/3/67 (Item 7 from file: 5) BIOSIS Number: 87103675 7043154 FLP RECOMBINASE OF THE 2 MUM CIRCLE PLASMID OF SACCHAROMYCES-CELEVISIAE BENDS ITS DNA TARGET ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BEHDING SCHWARTZ C J E; SADOWSKI P D DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN. J MOL BIOL 205 (4). 1989. 647-658. CODEN: JMOBA Full Journal Title: Journal of Molecular Biology Language: ENGLISH 2/3/68 (Item 8 from file: 5) BIOSIS Number: 87004981 HIGH FREQUENCY FLF-INDEPENDENT HOMOLOGOUS DNA RECOMBINATION OF 2 MICRON PLASMID IN THE YEAST SACCHAROMYCES-CEREVISIAE BRUSCHI C V; HOWE G A DEP. MICROBIOL. IMMUNOL., SCH. MED., EAST CAROLINA UNIV., GREENVILLE, N.C. 27858-4354, U.S.A. CURR GENET 14 (3). 1988. 191-200. CODEN: CUGED Full Journal Title: Current Genetics

Language: ENGLISH

2/3/69 (Item 9 from file: 5)

6892306 BIOSIS Number: 37086685

THE FLP RECOMBINASE STEP-ARREST MUTANTS AND INTERMEDIATES IN RECOMBINATION

JAYARAM M; PARSONS R; EVANS B

RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037.

SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION HELD AT THE 18TH ANNUAL UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELE:) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, STEAMBOAT SPRINGS, CO.ORADO, USA, MARCH 27-APRIL 3, 1989. J CELL BIOCHEM SUPPL Ø (13 PART D). 989. 106. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/70 (Item 10 from file: 5)

6636107 BIOSIS Number: 86102658

AUTOREGULATION OF 2-MUM CIRCLE GENE EXPRESSION PROVIDES A MODEL FOR MAINTENANCE OF STABLE PLASMID COPY LEVELS

SOM T; ARMSTRONG K A; VOLKERT F C; BROACH J R

DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, NEW JERSEY 08:444.

CELL 52 (1). 1988. 27-38. CODEN: CELLB

Full Journal Title: Cell

Language: ENGLISH

2/3/71 (Item 11 from file: 5)

6624830 BIOSIS Number: 86091381

THE INT FAMILY OF SITE-SPECIFIC RECOMBINASES SOME THOUGHTS ON A GENERAL REACTION MECHANISM

JAYARAM M

DEF. MOL. BIOL., RES. INST. SCRIFFS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J GENET 67 (1). 1988. 29-36. CODEN: JOGNA

Full Journal Title: Journal of Genetics

Language: ENGLISH

2/3/72 (Item 12 from file: 5)

6571174 BIOSIS Number: 86037725

FLP RECOMBINASE INDUCTION OF THE BREAKAGE-FUSION-BRIDGE CYCLE AND GENE CONVERSION IN SACCHAROMYCES-CEREVISIAE

RANK G H; XIAO W; KOLENOVSKY A; ARNDT G

DEP. BIOL., UNIV. SASK., SASKATOON, SASK., CAN. S7N OWO.

CURR GENET 13 (4). 1988. 273-282. CODEN: CUGED

Full Journal Title: Current Genetics

Language: ENGLISH

2/3/73 (Item 13 from file: 5)

6150196 BIOSIS Number: 35015717

PURIFICATION OF FLP RECOMBINASE USING SEQUENCE-SPECIFIC DNA AFF NITY CHROMATOGRAPHY

GATES C A; MEYER-LEON L; ATTWOOD J M; WOOD E A; COX M M

DEP. BIOCHEM., UNIV. WIS.-MADISON, MADISON, WIS. 53706, USA.

BURGESS, R. (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) GYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 68. PROTEIN PURIFICATION: MICRO TO MACRO; CETUS-UCLA SYMPOSIUM, FRISCO, COLORADO, USA, MARCH 29-APRIL 4, 1987. XVIII+510P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2667-9. 0 (0). 1987. 197-206. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/74 (Item 14 from file: 5)

5802738 BIOSIS Number: 83065045

SUBSTRATE RECOGNITION BY THE 2-MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE EFFECT OF MUTATIONS WITHIN THE SYMMETRY ELEMENTS OF THE MINIMAL SUBSTRATE

PRASAD P V; HORENSKY D; YOUNG L-J; JAYARAM M

DEP. MOL. BIOL., RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037, USA.

MOL CELL BIOL 6 (12). 1986. 4329-4334. CODEN: MCEBD

Full Journal Title: Molecular and Cellular Biology

Language: ENGLISH

2/3/75 (Item 15 from file: 5)

5761770 BIOSIS Number: 83024077

MATING TYPE-LIKE CONVERSION PROMOTED BY THE 2 MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE IMPLICATIONS FOR THE DOUBLE-STRAND-GAP REPAIR MODEL

JAYARAM M

DEP. MOLECULAR BIOLOGY, RESEARCH INST. SCRIPPS CLINIC, LA JOLLA, CALIFORNIA 92037.

MOL CELL BIOL 6 (11). 1986. 3831-3837. CODEN: MCERD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/76 (Item 16 from file: 5)

5751545 BIOSIS Number: 83013852

ASSOCIATION OF RECIPROCAL EXCHANGE WITH GENE CONVERSION BETWEEN THE REPEATED SEGMENTS OF 2-MICROMETER CIRCLE

JAYARAM M

DEPARTMENT OF MOLECULAR BIOLOGY, RESEARCH INSTITUTE OF SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J MOL BIOL 191 (3). 1986. 341-354. CODEN: JMORA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/77 (Item 17 from file: 5)

5696494 BIOSIS Number: 33091515

MECHANISMS OF ACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; BEATTY L G; CLARY D; OLLERHEAD S

DEP. MED. GENETICS, MED. SCIENCES BUILD., UNIV. TORONTO, TORONTO, CANADA M5S 1A8.

MCMACKEN, R. AND T. J. KELLY (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 47. DNA REPLICATION AND RECOMBINATION; PARK CITY, UTAH, USA, MARCH 16-23, 1986. XXVI+782P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2646-6. 0 (0). 1987. 691-702. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/78 (Item 18 from file: 5)

5504855 BIOSIS Number: 32027162

INTERACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID WITH ITS TARGET SEQUENCE

SADOWSKI P D; ANDREWS B J; BEATTY L G; SIDENBERG D; PROTEAU G DEP. MED. GENETICS, UNIV. TORONTO, TORONTO M5S 1A8. CAN.

KLAR, A. AND J. N. STRATHERN (ED.). CURRENT COMMUNICATIONS IN MOLECULAR BIOLOGY: MECHANISMS OF YEAST RECOMBINATION; MEETING, COLD SPRING HARBOR, N.Y., USA. IX+193F. COLD SPRING HARBOR LABORATORY: COLD SPRING HARBOR, N.Y., USA. ILLUS. PAPER. ISBN 0-87969-195-6. 0 (0). 1986. 7-10. CODEN: 24607

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/79 (Item 19 from file: 5)

5426144 BIOSIS Number: 82070947

INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID WITH MUTATED TARGET SEQUENCES

ANDREWS & J; MCLEOD M; BROACH J; SADOWSKI P D

DEF. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO, ONTARIO M5S 1A8, CANADA.

MOL CELL BIOL 6 (7). 1986. 2482-2489. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/80 (Item 20 from file: 5) 5389362 BIOSIS Number: 82034165

FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MICROMETER PLASMID TOPOLOGICAL FEATURES OF THE REACTION

BEATTY L G; BABINEAU-CLARY D; HOGREFE C; SADOWSKI P D
DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO M5S 1A8, CANADA.
J MOL BIOL 188 (4). 1986. 529-544. CODEN: JMOBA
Full Journal Title: Journal of Molecular Biology
Language: ENGLISH

2/3/81 (Item 21 from file: 5)

5265813 BIOSIS Number: 81033120

THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

GRONOSTAJSKI R M; SADOWSKI P D

DEP. MED. GENET., UNIV. TORONTO, TORONTO, ONT. M5S1A8, CAN. MOL CELL BIOL 5 (11). 1985. 3274-3279. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/82 (Item 22 from file: 5) 5256098 BIOSIS Number: 81023405

THE FLP PROTEIN OF THE 2-MICRON PLASMID OF YEAST SACCHAROMYCES-CEREVISIAE PURIFICATION OF THE PROTEIN FROM ESCHERICHIA-COLI CELLS EXPRESSING THE CLONED FLP GENE

BABINEAU D; VETTER D; ANDREWS B J; GRONOSTAJSKI R M; PROTEAU G A; BEATTY L G; SADOWSKI P D

DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, M5S 1A8, CANADA.

J BIOL CHEM 260 (22). 1985. 12313-12319. CODEN: JBCHA Full Journal Title: Journal of Biological Chemistry Language: ENGLISH

2/3/83 (Item 23 from file: 5) 5168213 BIOSIS Number: 31057528

THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; ANDREWS B J; BABINEAU-CLARY D; BEATTY L; GRONOSTAJSKI R M; FROTEAU G; SIDENBERG D

DEP. MED. GENET., UNIV. TORONTO, TORONTO M5S 1A8, CANADA.

SYMPOSIUM ON MECHANISMS OF DNA REPLICATION AND RECOMBINATION HELD AT THE 15TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, MAR. 16-23, 1986. J CELL BIOCHEM SUPPL 0 (10 PART B). 1986. 137. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/84 (Item 24 from file: 5) 4696890 BIOSIS Number: 29054205

INTERACTION OF THE FLP RECOMBINASE WITH SUBSTRATE 2-MICRON CIRCLE DNA ANDREWS & J; BEATTY L; SADOWSKI P D UNIV. TORONTO.

SYMPOSIUM ON YEAST CELL BIOLOGY HELD AT THE 14TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA - LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, APR. 9-15, 1985. J CELL BIOCHEM SUPPL Ø (9 PART C). 1985. 117. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/85 (Item 1 from file: 399)

116167825 CA: 116(17)167825y PATENT

Methods for in vitro recombination of multigene families for generation of new phenotypes

INVENTOR (AUTHOR): Short, Jay M.; Sorge, Joseph A.

LOCATION: USA

ASSIGNEE: Stratagene

PATENT: PCT International; WO 9116427 A1 DATE: 911031 APPLICATION: WO 91US2910 (910424) *US 513957 (900424)

PAGES: 204 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/00A; C12P-019/34B; C12P-021/06B; C07H-021/00B DESIGNATED COUNTRIES: AU; CA; FI; JP; KR; NO DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE

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2/3/86 (Item 2 from file: 399)

106208826 CA: 106(25)208826p JOURNAL

Rapid localization and characterization of random mutations within the 2.mu. circle site-specific recombinase: a general strategy for analysis of protein function

AUTHOR(S): Govind, Nadathur S.; Jayaram, Makkuni LOCATION: Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA JOURNAL: Gene DATE: 1987 VOLUME: 51 NUMBER: 1 PAGES: 31-41 CODEN: GENEDG ISSN: 0378-1119 LANGUAGE: English Copyright 1992 by the American Chemical Society

2/3/87 (Item 3 from file: 399)

104001445 CA: 104(1)1445b JOURNAL

The FLP recombinase of the yeast 2-.mu.m plasmid: characterization of its recombination site

AUTHOR(S): Senecoff, Julie F.; Bruckner, Robert C.; Cox, Michael M. LOCATION: Coll. Agric. Life Sci., Univ. Wisconsin, Madison, WI, 53706, USA

JOURNAL: Proc. Natl. Acad. Sci. U. S. A. DATE: 1985 VOLUME: 62 NUMBER: 21 PAGES: 7270-4 CODEN: PNASA6 ISSN: 0027-8424 LANGUAGE: English

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2/3/88 (Item 4 from file: 399)

102216080 CA: 102(25)216080y JOURNAL

The FLP recombinase of the 2.mu. circle DNA of yeast: interaction with its target sequences

AUTHOR(S): Andrews, Brenda J.; Proteau, Gerald A.; Beatty, Linda G.; Sadowski, Paul D.

LOCATION: Dep. Med. Genet., Univ. Toronto, Toronto, ON, Can., M5S 1A8 JOURNAL: Cell (Cambridge, Mass.) DATE: 1985 VOLUME: 40 NUMBER: 4 PAGES: 795-803 CODEN: CELLB5 ISSN: 0092-8674 LANGUAGE: English

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2/3/89 (Item 1 from file: 434)

11609410 Genuine Article#: HX635 No. References: 12

Title: HALF-SITE STRAND TRANSFER BY STEP-ARREST MUTANTS OF YEAST SITE-SPECIFIC RECOMBINASE FLP

Author(s): SERRE MC: JAYARAM M

Corporate Source: UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712; UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N3 (JUN 5), P643-649 Language: ENGLISH Document Type: ARTICLE

2/3/90 (Item 2 from file: 434)

11609409 Genuine Article#: HX635 No. References: 25

Title: HALF-SITE RECOMBINATIONS MEDIATED BY YEAST SITE-SPECIFIC RECOMBINASE-FLP AND RECOMBINASE-R

Author(s): SERRE MC; EVANS BR; ARAKI H; OSHIMA Y; JAYARAM M

Componate Sounce: UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712; UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712; OSAKA UNIV, FAC ENGN, DEPT FERMENTAT TECHNOL/SUITA/OSAKA 565/JAPAN/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N3 (JUN 5), P321-642 Language: ENGLISH Document Type: ARTICLE

2/3/91 (Item 3 from file: 434)

11603498 Genuine Article#: HX080 No. References: 40

Title: MUTAGENESIS OF A CONSERVED REGION OF THE GENE ENCODING THE FLP RECOMBINASE OF SACCHAROMYCES-CEREVISIAE - A ROLE FOR ARGININE-191 IN BINDING AND LIGATION

Author(s): FRIESEN H: SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/; UNIV TORONTO, DEFT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N2 (MAY 20), P313-326 Language: ENGLISH Document Type: ARTICLE 2/3/92 (Item 4 from file: 434) 11588831 Genuine Article#: HV855 No. References: 41 Title: SITE-SPECIFIC RECOMBINASE, R, ENCODED BY YEAST PLASMID PSR1 Author(s): ARAKI H; NAKANISHI N; EVANS BR; MATSUZAKI H; JAYARAM M; OSHIMA Y Corporate Source: OSAKA UNIV, FAC ENGN, DEPT BIOTECHNOL, 2-1 YAMADAOKA/SUITA/OSAKA 565/JAPAN/; OSAKA UNIV, FAC ENGN, DEPT BIOTECHNOL, 2-1 YAMADAOKA/SUITA/OSAKA 565/JAPAN/; UNIV TEXAS, DEFT MICROBIOL/AUSTIN//TX/78712 Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N1 (MAY 5), P25-37 Language: ENGLISH Document Type: ARTICLE 2/3/93 (Item 5 from file: 434) 11506141 Genuine Article#: HN234 No. References: 35 Title: SITE-SPECIFIC RECOMBINATION OF 2-MU-M PLASMID OF YEAST SACCHAROMYCES-CEREVISIAE Author(s): PUSHNOVA EA Corporate Source: ST PETERBURG PEDIAT MED INST/ST PETERBURG//USSR/ Journal: GENETIKA, 1992, V28, N2 (FEB), P25-34 Language: RUSSIAN Document Type: ARTICLE (Abstract Available) 2/3/94 (Item & from file: 434) 11487805 Genuine Article#: HM053 No. References: 33 Title: SITE-SPECIFIC INTEGRATION OF THE HAEMOPHILUS-INFLUENZAE BACTERIOPHAGE HP1 - IDENTIFICATION OF THE POINTS OF RECOMBINATIONAL STRAND EXCHANGE AND THE LIMITS OF THE HOST ATTACHMENT SITE Author(s): HAUSER MA; SCOCCA JJ Corporate Source: JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205; JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205 Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N10 (APR 5), P 6859-6864 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/95 (Item 7 from file: 434) 11338662 Genuine Article#: HB304 No. References: 21 Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED Y THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM Author(s): BAYLEY CC; MORGAN M; DALE EC; OW DW Corporate Source: USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800'BUC: ANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY, DEPT PLANT PATHOL/BERKELEY//CA/94720 Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361 Language: ENGLISH

2/3/96 (Item 8 from file: 434) 11317754 Genuine Article#: GZ516 No. References: 33

Document Type: ARTICLE (Abstract Available

Title: A FROG VIRUS-3 GENE CODES FOR A PROTEIN CONTAINING THE MOTIF CHARACTERISTIC OF THE INT FAMILY OF INTEGRASES Author(s): ROHOZINSKI J; GOORHA R Corporate Source: ST JUDE CHILDRENS HOSP, DEFT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101; ST JUDE CHILDRENS HOSP, DEPT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101 Journal: VIROLOGY, 1992, V186, N2 (FEB), P693-700 Language: ENGLISH Document Type: ARTICLE 2/3/97 (Item 9 from file: 434) 10583597 Genuine Article#: EP811 No. References: 61 Title: A NOVEL RECOMBINATOR IN YEAST BASED ON GENE-II PROTEIN FROM BACTERIOFHAGE-F1 Author(s): STRATHERN JN; WEINSTOCK KG; HIGGINS DR; MCGILL CB Corporate Source: NCI, FREDERICK CANC RES & DEV CTR, BASIC RES PROGRAM/FREDERICK//MD/21701 Journal: GENETICS, 1991, V127, N1, P61-73 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/98 (Item 10 from file: 434) 09323349 Genuine Article#: T4208 No. References: 45 Title: FLP RECOMBINASE OF THE 2-MU-M CIRCLE PLASMID OF SACCHAROMYCES-CEREVISIAE BENDS ITS DNA TARGET - ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BENDING Author(s): SCHWARTZ CJE: SADOWSKI FD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1989, V205, N/, P647-658 Language: ENGLISH Document Type: ARTICLE 2/3/99 (Item 11 from file: 434) 07863892 Genuine Article#: F8861 No. References: 37 Title: ISOLATION OF INTERMEDIATES IN THE BINDING OF THE FLP RECOMBINASE OF THE YEAST PLASMID 2-MIRON CIRCLE TO ITS TARGET SEQUENCE Author(s): ANDREWS BJ; BEATTY LG; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1987, V193, N2, P345-358 Language: ENGLISH Document Type: ARTICLE (Item 12 from file: 434) 2/3/100 07372665 Genuine Article#: C9356 No. References: 23 Title: INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M FLASMID WITH MUTATED TARGET SEQUENCES Author(s): ANDREWS BJ; MCLEOD M; BROACH J; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/; COLD SPRING HARBOR LAB/COLD SPRING . HARBOR//NY/11724; PRINCETON UNIV, DEPT MOLEC BIOL/PRINCETON//NJ/08544 Journal: MOLECULAR AND CELLULAR BIOLOGY, 1986, V6, N7, P2482-2489 Language: ENGLISH Document Type: ARTICLE (Item 13 from file: 434) 2/3/101

07260459 Genuine Article#: C1205 No. References: 44
Title: FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MU-M PLASMID - TOPOLOGICAL

FEATURES OF THE REACTION

Author(s): BEATTY LG; BABINEAUCLARY D; HOGREFE C; SADOWSKI FD

Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1986, V188, N4, F529-544

Language: ENGLISH Document Type: ARTICLE

2/3/102 (Item 14 from file: 434)

06806789 Genuine Article#: AUF29 No. References: 22

Title: THE FLP RECOMBINASE OF THE YEAST 2-MU-M PLASMID - CHARACTERIZATION OF ITS RECOMBINATION SITE

Author(s): SENECOFF JF; BRUCKNER RC; COX MM

Corporate Source: UNIV WISCONSIN, COLL AGR & LIFE SCI, DEFT BIOCHEM, 420 HENRY MALL/MADISON//WI/53706

Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 1985, V82, N21, P7270-7274

Language: ENGLISH Document Type: ARTICLE

2/3/103 (Item 15 from file: 434)

06780315 Genuine Article#: ATE60 No. References: 28

Title: THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

Author(s): GRONOSTAJSKI RM; SADOWSKI PD

Corporate Source: UNIV TORONTO, DEFT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/

Journal: MOLECULAR AND CELLULAR BIOLOGY, 1985, V5, N11, P3274-3279 Language: ENGLISH Document Type: ARTICLE

2/3/104 (Item 1 from file: 440)

03761331 Genuine Article#: HZ483 No. References: 12

Title: LIGATION ACTIVITY OF FLP RECOMBINASE - THE STRAND LIGATION ACTIVITY OF A SITE-SPECIFIC RECOMBINASE USING AN ACTIVATED DNA SUBSTRATE

Author(s): PAN GH; SADOWSKI PDV(Reprint)

Corporate Source: UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/ (Reprint); UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N18 (JUN 25), P 12397-12399

Language: ENGLISH Document Type: NOTE (Abstract Available)

2/3/105 (Item 1 from file: 76)

1171271 82001618771

Mutations in the 2-.mu.m circle site-specific recombinase that abolish recombination without affecting substrate recognition.

Prasad, F.V.; Young, L.-J.; Jayaram, M.

Dep. Mol. Biol., Res. Inst. Scripps Clin., 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

PROC. NATL. ACAD. SCI. USA; 84(8), pp. 2189-2193 1987

Language: English Summary Language: English

2/3/106 (Item 1 from file: 73)

8210454 EMBASE No: 91239554

Erratum: Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination (Vol.

265 (1990) 18504-18510)

Evans B.R.; Chen J.-W.; Parsons R.L.; Bauer T.K.; Teplow D.B.; Jayaram M. J. BIOL. CHEM. (USA), 1991, 266/11 (7312) CODEN: JBCHA ISSN: 0021-9258

LANGUAGES: English

2/3/107 (Item 2 from file: 73)

7363228 EMBASE No: 89079376

FLP recombinase of the 2 microm circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending

Schwartz C.J.E.; Sadowski P.D.

Department of Medical Genetics, University of Toronto, Toronto, Ont. M5S

J. MOL. BIOL. (United Kingdom), 1989, 205/4 (647-658) CODEN: JMOBA ISSN: 0022-2836

LANGUAGES: English

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2/3/108 (Item 1 from file: 144)

09775158 PASCAL No.: 91-0572331

Domain of a yeast site-specific recombinase (Flp) that recognizes its target site

JING-WEN CHEN; EVANS B R; SANG-HWA YANG; TEPLOW D/ B; JAYARAM M Univ. Texas, dep. microbiology, Austin TX 78712, USA

Journal: Proceedings of the National Academy of Sciences of the United States of America, 1991, 88 (14) 5944-5948

Language: English

2/3/109 (Item 2 from file: 144)

09771721 FASCAL No.: 91-0568894

Protein-based assymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination

XIAO-HONG QIAN; INMAN R B; COX M M

Univ. Wisconsin, coll. agricultural life sci., dep. biochemistry, Madison WI 53706, USA

Journal: Journal of biological chemistry (The), 1990, 265 (35) 21779-21788

Language: English

2/3/110 (Item 3 from file: 144)

09730857 FASCAL No.: 91-0527991

Site-specific recombination between homologous chromosomes in Drosophila GOLIC K ${\sf G}$

Univ. Chicago, Howard Hughes medical inst., dep; molcular genetics cell biology, Chicago IL 60637, USA

Journal: Science: (Washington, DC), 1991, 252 (5008) 958-961 Language: English

2/3/111 (Item 4 from file: 144) 09563896 PASCAL No.: 91-0354326

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes: differential activity in full-site and half-site recombinations

JING-WEN CHEN; EVANS B R; LEI ZHENG; JAYARAM M

Univ. Texas at Austin, dep. microbiology, Austin TX 78712, USA Journal: Journal of molecular biology, 1991, 218 (1) 107-118 Language: English

2/3/112 (Item 5 from file: 144)

07823248 PASCAL No.: 87-0302971

Interaction of the FLP recombinase of the saccharomyces cerevisiae 2 mu m plasmid with mutated target sequences

NDREWS B J; MCLEOD M; BROACH J; SADOWSKI P D

Univ. Toronto, dep. medical genetics, Toronto ON M5S 1A8, Canada Journal: Molecular and cellular biology, 1986, 6 (7) 2482-2489 Language: ENGLISH

2/3/113 (Item 1 from file: 77) 89015048 V17N02

FLP recombinase induction of the breakage-fusion-bridge cycle (BFBC) and gene conversion in Saccharomyces cerevisiae

Rank, G.H.; Xiao, W.; Kolenovsky, A.; Arndt, G.

Univ. Saskatchewan, Saskatoon, Sask., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/114 (Item 2 from file: 77)

89014585 V17N02

Structure-function relationship of the sequence specific DNA binding function of the FLP recombinase

Amin, A.A.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Froceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/115 (Item 3 from file: 77)

89014584 V17N02

FLP recombinase of 2 mu circle of S. cerevisiae bends its DNA target: An in vitro analysis $\frac{1}{2}$

Schwartz, C.J.E.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/116 (Item 4 from file: 77) 89013277 V17N02 Mutational analysis of the FLP site-specific recombinase of the yeast 2 micron plasmid

Sadowski, P.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome

2/3/117 (Item 5 from file: 77)

89012894 V17N02

Step-arrest mutants of FLP recombinase: Implications for the mechanism of recombination

Evans, B.R.; Parsons, R.; Crain, K.; Jayaram, M.

Mol. Biol. Dep., Res. Inst. Scripps Clin. and Res. Found., La Jolla, CA,

14th International Conference on Yeast Genetics and Molecular Biology 8830578 Espoo (Finland) 7-13 Aug 1988

European Association for Cancer Research

Subscription Department C, John Wiley & Sons Inc., 605 Third Avenue, New York, NY 10158 (USA), Abstracts will be Published in Special Issue of Journal 'Yeast' Volume 4. ISSN 0749-503X

2/3/118 (Item 1 from file: 265)

0128688 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 5R01GM35654-07 AGENCY CODE: CRISP Site specific recombination in the yeast plasmid 2 micron circle PRINCIPAL INVESTIGATOR: JAYARAM, MAKKUNI ADDRESS: UNIVERSITY OF TEXAS DEPT OF MICROBIOLOGY AUSTIN, TX 78712 PERFORMING ORG.: UNIVERSITY OF TEXAS AUSTIN, AUSTIN, TEXAS SPONSORING ORG.: NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES FY: 92 FUNDS: \$265,024

2/3/119 (Item 2 from file: 265)

0092015 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS
IDENTIFYING NO.: 1R01HD28694-01 AGENCY CODE: CRISP
Site-specific recombination in spermatogenesis (Drosophila)
PRINCIPAL INVESTIGATOR: GOLIC, KENT G
ADDRESS: UNIVERSITY OF UTAH SALT LAKE CITY, UT 84112
PERFORMING ORG.: UNIVERSITY OF UTAH, SALT LAKE CITY, UTAH
SPONSORING ORG.: NATIONAL INSTITUTE OF CHILD HEALTH AND HUMAN DEVELOPMENT
FY: 92 FUNDS: \$152,007

2/3/120 (Item 3 from file: 265)

0019654 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS
IDENTIFYING NO.: 9105934; 9105934 AGENCY CODE: NSF
Genetic Analysis of Pattern Formation During Drosophila Neurogenesis
PRINCIPAL INVESTIGATOR: Ellis, Hilary M Dr.
PERFORMING ORG.: Emory University, Biology, Atlanta, GA 30322
PROJECT MONITOR: Data is not available
SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY
& NEUROSCIENC, Washington, D.C., 20550

DATES: 910715 TO 920630 FY: 91 FUNDS: \$69,613 (Item 4 from file: 265) 2/3/121 0019101 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 9103946; 9103946 AGENCY CODE: NSF Generation of Mosaicism in Mice by a Site-Specific Recombinase (FLP) PRINCIPAL INVESTIGATOR: O'Gorman, Stephen Dr. PERFORMING ORG.: Salk Institute for Biological Studies, Gene Expression Laboratory, San Diego, CA 92128 PROJECT MONITOR: Thomas E. Brady SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY & NEUROSCIENC, Washington, D.C., 20550 DATES: 910315 TO 920831 FY: 91 FUNDS: \$49,522 (Item 5 from file: 265) 2/3/122 0016053 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS . IDENTIFYING NO.: 9019220; 9019220 AGENCY CODE: NSF Genetic Analysis in Arabidopsis PRINCIPAL INVESTIGATOR: Signer, Ethan R Dr. PERFORMING Massachusetts Institute of Technology, Biology, ORG.: Cambridge, MA 02139 PROJECT MONITOR: DeLill Nasser SPONSORING ORG.: National Science Foundation, DIV OF MOLECULAR & CELLULAR BIOSCIENCES, Washington, D.C., 20550 DATES: 910201 TO 930731 FY: 91 FUNDS: \$200,000 2/3/123 (Item 1 from file: 35) 01212062 ORDER NO: AADNN-59965 THE ROLE OF DNA BENDING IN FLP-MEDIATED SITE-SPECIFIC RECOMBINATION Author: SCHWARTZ, CAROL JUDITH ELAINE Degree: PH.D. Year: 1990 Corporate Source/Institution: UNIVERSITY OF TORONTO (CANADA) (0779) Source: VOLUME 52/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 5647. 209 PAGES ISBN: 0-315-59965-0 2/3/124 (Item 2 from file: 35) 01142876 ORDER NO: AAD90-30816 UNUSUAL DNA STRUCTURE IN SITE-SPECIFIC AND HOMOLOGOUS RECOMBINATION (RECOMBINATION) Author: UMLAUF, SCOTT W. Degree: PH.D. Year: 1990 Corporate Source/Institution: THE UNIVERSITY OF WISCONSIN - MADISON (Source: VOLUME 51/09-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 4199. 219 PAGES 2/3/125 (Item 3 from file: 35) 1061565 ORDER NO: AAD89-12817

ANALYSIS OF THE MAJOR DNASE I HYPERSENSITIVE SITE ON THE YEAST TWO-MICRON

DNA PLASMID

Author: STRAND, ANDREW DAVID

Degree: FH.D. Year: 1989

Corporate Bource/Institution: UNIVERBITY OF MINHEBOTA (U130) Source: VOLUME 50/02-B OF DISSERTATION ABSTRACTS INTERNATIONAL.

PAGE 446. 111 PAGES

2/3/126 (Item 4 from file: 35)

949308 ORDER NO: AAD87-06690

A GENETIC ANALYSIS OF FACTORS INVOLVED IN THE MAINTENANCE OF THE 2 MICRON PLASMID OF SACCHAROMYCES CEREVISIAE (CHROMATIN)

Author: VEIT, BRUCE EDWARD

Degree: PH.D. Year: 1986

Corporate Source/Institution: UNIVERSITY OF WASHINGTON (0250)
Source: VOLUME 47/12-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 4763. 97 PAGES

2/3/127 (Item 1 from file: 51) 00405585 91-03-b0028 SURFILE: FSTA

Yeast 2 MUm vectors replicate and undergo recombination in Torulaspora delbrueckii.

Compagno, C.; Ranzi, B. M.; Martegani, E.

Correspondence (Reprint) address, B. M. Ranzi, Dipartimento di Fisiologia e Biochimica Generali, Sezione di Biochimica Comparata, Univ. di Milano, Milan, Italy

Molecular Microbiology 1989 , 3 (8) 1003-1010 LANGUAGE: English

2/3/128 (Item 1 from file: 60)

09154644

PROJ NO: NYC-186301 AGENCY : SAES NY.C

PROJ TYPE: STATE

START: 01 JUL 91 TERM: 30 JUN 92

INVEST: MACINTYRE R J

ENTOMOLOGY

CORNELL UNIVERSITY ITHACA NEW YORK 14853

DEVELOPMENT OF A MORE EFFICIENT INSECT TRANSFORMATION SYSTEM

OBJECTIVES: The goal of the research described below is to develop a system in which DNA canbe both easily and effectively delivered to insect embryos and, using the yeast "flip recombinase" system, insure the recovery of transgenic animals at high frequencies.

PRIMARY HEADINGS: R207 Insect Control-Field Crops; A4500 Protection Against Insects; C6500 Invertebrates; F1313 Physiology-Other

2/3/129 (Item 2 from file: 60)

09091400

PROJ NO: WISØ2827 AGENCY : SAES WIS

PROJ TYPE: STATE

START: 01 JUL 86 TERM: 30 NOV 96 FY: 1989

INVEST: COX M M

BIOCHEMISTRY UNIV OF WISCONSIN MADISON WISCONSIN 53706

?t3/3/1-3

THE BIOCHEMISTRY OF GENETIC RECOMBINATION

OBJECTIVES: The FLP recombinase (derived from yeast) has been purified extensively. The properties of this protein and the recombination event it catalyzes are being studied in vitro. The recombination site utilized by this protein has been defined in detail. Studies on the mechanism of action of this recombination system are now getting underway.

PRIMARY HEADINGS: R318 Noncommodity Biotechnology, Biometry; A7000 Experimental Design, Statistical Methods; C6300 Biological Cell Systems; F0114 Biochemistry and Biophysics-Other

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2/3/130
             (Item 1 from file: 286)
0050984
          Journal Announcement: 08APR91 Doc Type: 2
  Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355
1ST COMPANY/ORGANIZATION NAME:
  Salk Institute for Biological Studies, The, USA (1921)
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3/3/1 (Item 1 from file: 155)

07645850 91164850

Recombinase-mediated gene activation and site-specific integration in mammalian cells.

O'Gorman S; Fox DT; Wahl GM

Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

Science Mar 15 1991, 251 (4999) p1351-5, ISSN 0036-8075

Journal Code: UJ7 Languages: ENGLISH

Document type: JOURNAL ARTICLE

3/3/2 (Item 1 from file: 434)

11338662 Genuine Article#: HB304 No. References: 21

Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM

Author(s): BAYLEY CC; MORGAN M; DALE EC: OW DW

Corporate Source: USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY,DEPT PLANT PATHOL/BERKELEY//CA/94720

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361 Language: ENGLISH Document Type: ARTICLE (Abstract Available)

3/3/3 (Item 1 from file: 286) 0050984 Journal Announcement: 08APR91 Doc Type: 2 Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355

1ST COMPANY/ORGANIZATION NAME:

Salk Institute for Biological Studies, Th., USA (1921) ?t3/4/1-3

3/4/1 (Item 1 from file: 155)

FN- DIALOG MEDLINE file 155

AN- 076458501

AN- (NLM) 911648501

TI- Recombinase-mediated gene activation and site-specific integration in mammalian cells.

AU- Q'Gorman S; Fox DT; Wahl GMI

CS- Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

JN- Science; 251 (4999) p1351-51

PY- Mar 15 19911

SN- 0036-80751

JC- UJ71

LA- ENGLISHI

DT- JOURNAL ARTICLE!

JA- 91061

SF- INDEX MEDICUS!

AB- A binary system for gene activation and site-specific integration, based on the conditional recombination of transfected sequences mediated by the FLP recombinase from yeast, was implemented in mammalian cells. In several cell lines, FLP rapidly and precisely

recombined copies of its specific target sequence to activate an otherwise silent beta-galactosidase reporter gene. Clones of marked cells were generated by excisional recombination within a chromosomally integrated copy of the silent reporter. By the reverse reaction, integration of transfected DNA was targeted to a specific chromosomal site. The results suggest that FLP could be used to mosaically activate or inactivate transgenes for analysis of vertebrate development, and to efficiently integrate transfected DNA at predetermined chromosomal locations.

GS- Animal; In Vitro; Support, Non-U.S. Gov'tl

DE- *DNA Nucleotidyltransferases -- Metabolism -- ME;

**Mammals -- Genetics -- GE; **Recombination, Genetic; **Transfection;

beta-Galactosidase -- Genetics -- GE; *Animals, Transgenic; *Cell Line;

**DNA Nucleotidyltransferases -- Genetics -- GE; *Restriction Mapping!

ID- EC 2.7.7.- (DNA Nucleotidyltransferases); EC 2.7.7.- (FLP recombinase); EC 3.2.1.23 (beta-Galactosidase);

ID- FLP1

3/4/2 (Item 1 from file: 434)

FN- SCISEARCH 1974 - 9206W3

AN- 113386621

GA- HB3041

TI- EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM!

LA- ENGLISHI

AU- BAYLEY CC; MORGAN M; DALE EC; OW DWI

CS- USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY,DEPT PLANT PATHOL/BERKELEY//CA/94720|

GL - TISAT

JN- FLANT MOLECULAR BIOLOGY, 1992, V18, N2, F353-3611

PY- 19921

DT- ARTICLE!

NR- 211

SF- SciSearch; CC LIFE--Current Contents, Life Sciences; CC AGRI--Current Contents, Agriculture, Biology & Environmental Sciences!

SC- BOTANY; BIOCHEMISTRY & MOLECULAR BIOLOGY!

- AB- The Cre-lox site-specific recombination system of bacteriophage P1 was used to excise a firefly luciferase (luc) gene which had previously been incorporated into the tobacco genome. The excision event was due to site-specific DNA recombination between two lox sequences flanking the luc gene and was catalyzed by the Cre recombinase introduced by cross-fertilization. Recombination resulted in the fusion of a promoter with a distally located hygromycin phosphotransferase (hpt) coding sequence and the excision event was monitored as a phenotypic change from expression of luc to expression of hpt. The efficiency of recombination was estimated from the exchange of gene activity and confirmed by molecular analysis. The relevance to potential applications of site-specific deletion-fusion events for chromosome engineering are discussed.
- DE- Author Keywords: GENETIC ENGINEERING; PHAGE P1; RECOMBINASE; LUCIFERASE; SELECTABLE MARKERS!
- ID- KeyWords Flus: FIREFLY LUCIFERASE GENE; FLP RECOMBINASE;
 MAMMALIAN-CELLS; 2-MU CIRCLE; DNA; YEAST; BACTERIOPHAGE-P1;

GENOME: EXPRESSION: SEQUENCES! (TRANSGENIC PLANTS; TRANSIENT EXPRESSION OF THE GUS GENE; RF- 90-0047 002 INDICA RICE PROTOPLASTS; MICROPROJECTILE BOMBARDMENT; AGROBACTERIUM MEDIATED TRANSFORMATION) 90-1257 001 (BACILLUS-THURINGIENSIS STRAINS; TRANSGENIC TOBACCO PLANTS; DRY BEANS (PHASEOLUS-VULGARIS L); EXPRESSION OF INSECTICIDAL ACTIVITY: INSECT MIDGUT) 90-2362 001 (STA58 MAJOR ANTIGEN GENE; RHODOCOCCUS-FASCIANS CLONING VECTORS; ESCHERICHIA-COLI CHROMOCOME; PRECISE IDENTIFICATION) 90-4791 001 (FIREFLY LUCIFERASE EXPRESSION IN TRANSGENIC PLANTS; PROTEIN OF MAIZE TRANSPOSABLE ELEMENT AC; CAULIFLOWER MOSAIC-VIRUS; REPORTER GENES) 90-7783 001 (POLYMERASE CHAIN-REACTION; DNA AMPLIFICATION; POLYMORPHIC NUCLEOTIDE SUBSTITUTIONS IN JETA-GLOBIN GENES) CR - ANDREWS BJ, 1985, V40, P795, CELL BEVAN M, 1984, V12, P8711, NUCLEIC ACIDS RES BROACH JR, 1980, V21, P501, CELL CRAIG NL, 1988, V22, P77, ANNU REV GENET DALE EC, 1990, V91, P79, GENE DEWET JR, 1987, V7, P725, MOL CELL BIOL GOLIC KG, 1989, V59, P499, CELL HOESS RH, 1985, V181, P351, J MOL BIOL HORSCH RB, 1985, V227, F1229, SCIENCE KASTER KR, 1983, V11, P6895, NUCLEIC ACIDS RES MANIATIS T, 1982, MOL CLONING ODELL J, 1990, V223, P369, MOL GEN GENET OGORMAN S, 1991, V251, P1351, SCIENCE

VERWOERD TC, 1989, V17, P2362, NUCLEIC ACIDS RESIDENTED A

STERNBERG N. 1981, V150, P467, J MOL BIO!

SAUER B, 1989, V17, P147, NUCLEIC ACIDS LES SAUER B, 1988, V85, P5166, P NATL ACAD SCI USA SENECOFF JF, 1985, V82, P7270, P NATL ACAD SCI USA

OW DW, 1986, V234, P856, SCIENCE SAIKI RK, 1988, V239, P487, SCIENCE

VAECK M, 1987, V328, P33, NATURE

AP - 00509841

JA- 08APR911

DT- 21

JN- Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-13551

AF- Salk Institute scientists have shown that the site specific recombinase enzyme, FLP, from Saccharomyces cere isiae can be used for gene activation in mammalian cells and have suggested it may be useful to mosaically inactivate or activate transgenes or to efficiently integrate transfected DNA at predetermined chromosomal locations.

 $C^{m_{\rm m}}$ Salk Institute for Biological Studies, The, USA (1921)!

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=> d his

(FILE 'USPAT' ENTERED AT 09:57:49 ON 12 JUL 94) SET PAGELENGTH SCROLL

L1 5 S (YEAST? OR CEREVISIAE?)(30A)(FRT OR FLP OR RECOMBINASE?)

=> d 1-5

- 1. 5,268,296, Dec. 7, 1993, DNA vector and recombinant host cell for production of hirullin P6 and P18; Reinhard Maschler, et al., 435/252.3, 69.1, 172.3, 320.1, 942; 536/23.5 [IMAGE AVAILABLE]
- 2. 5,268,285, Dec. 7, 1993, Strains of yeast with increased rates of glycolysis; David T. Rogers, et al., 435/172.3, 161, 194, 254.21, 320.1 [IMAGE AVAILABLE]
- 3. 5,227,288, Jul. 13, 1993, DNA sequencing vector with reversible insert; Frederick R. Blattner, 435/6, 252.3, 252.33, 320.1; 935/29, 72, 73 [IMAGE AVAILABLE]
- 4. 5,114,922, May 19, 1992, Polypeptides with an anticoagulant activity; Reinhard Maschler, et al., 514/12; 530/324 [IMAGE AVAILABLE]
- 5. 4,997,757, Mar. 5, 1991, Process for detecting potential carcinogens; Robert H. Schiestl, 435/172.1, 6, 29, 172.3; 935/76, 78, 79, 84 [IMAGE AVAILABLE]

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=> d his 12

(FILE 'USPAT' ENTERED AT 09:57:49 ON 12 JUL 94)
L2 LS MAMMAL?(100A)(FRT OR FLP OR RECOMBINASE?)

⇔ d kwie

US PAT NO: 5,159,066 [IMAGE AVAILABLE]

L2: 1 of 1

ABSTRACT:

Recombination activating gene of mammalian origin (RAG-1), cDNA of RAG-1 of mammalian origin, mRNA expressed by RAG-1, the encoded recombinase and antibodies specific for the recombinase, as well as the use of the same for a diagnostic or therapeutic purpose.

DETDESC:

DETD(2)

The present invention relates to a gene of mammalian origin, referred to as recombination activating gene or RAG-1, which confers the ability to carry out V(D)J recombination on cells in which it is expressed. The RAG-1 gene product is thus a direct or indirect activator of V(D)J recombinase activity. The invention also refers to RAG-1 mRNA and to the RAG-1 encoded product. RAG-1 has been shown in pre-B. . . as in all transfectants into which it has been introduced. This pattern of expression is that expected for the V(D)J recombinase and, therefore, RAG-1 appears to be a master controller of the development of the effector cells of the immune system. .

CLAIMS:

CLMS(3)

3. Isolated DNA of mammalian origin encoding recombinase.

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=> d his
  (FILE 'USPAT' ENTERED AT 14:51:48 ON 03 FEB 94)
       SET PAGELENGTH SCROLL
       0 S MAMMAL?(20A)(FLP OR FRT)(20A)(TRANSFECT? OR TRANSFORM? OR R
L1
L2
       5 S YEAST(20A)(FRT OR FLP)
L3
       0 S MAMMAL?(50A)(FLP OR FRT)
L4
       0 S MAMMAL?(100A)(FRT OR FLP)
L5
       0 S MAMMAL(50A)(YEAST OR CEREVISIAE)(50A)RECOMBINASE?
L6
       0 S MAMMAL?(200A)(YEAST? OR FUNG? OR CEREVISIAE)(200A)RECOMBINA
=> file jpoabs
FILE 'JPOABS' ENTERED AT 14:58:17 ON 03 FEB 94
    JAPANESE PATENT ABSTRACTS
 * CURRENTLY, DATA IS LOADED THROUGH THE ABSTRACT PUBLICATION *
 * DATE OF JULY 5, 1993
 * THE LATEST GROUPS RECEIVED ARE: C1078 E1392, M1438 & P1567. *
=> s l1
     769 MAMMAL?
     21 FLP
     12 FRT
     32 TRANSFECT?
    39194 TRANSFORM?
    2791 RECOMB?
       0 MAMMAL?(20A)(FLP OR FRT)(20A)(TRANSFECT? OR TRANSFORM? OR RECO
L7
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    2510 YEAST
     12 FRT
     21 FLP
L8
       0 YEAST(20A)(FRT OR FLP)
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     769 MAMMAL?
     21 FLP
      12 FRT
L9
       0 MAMMAL?(50A)(FLP OR FRT)
=> s |4
     769 MAMMAL?
     12 FRT
     21 FLP
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L10

0 MAMMAL?(100A)(FRT OR FLP)

=> s I5
355 MAMMAL
2510 YEAST
278 CEREVISIAE
0 RECOMBINASE?
L11 0 MAMMAL(50A)(YEAST OR CEREVISIAE)(50A)RECOMBINASE?

=> log y U.S. Patent & Trademark Office LOGOFF AT 14:58:54 ON 03 FEB 94 mammal? (100 N)(FLP or FRT)

DIAL OBJECT OF OPPORT

? t2/7/1-16

2/7/1 (Item 1 from file: 434)

12729441 Genuine Article#: MK280 Number of References: 51

Title: SITE-SPECIFIC RECOMBINASES - TOOLS FOR GENOME ENGINEERING

Author(s): KILBY NJ; SNAITH MR; MURRAY JAH

Corporate Source: UNIV CAMBRIDGE, INST BIOTECHNOL, TENNIS COURT

RD/CAMBRIDGE

CB2 1QT//ENGLAND/

Journal: TRENDS IN GENETICS, 1993, V9, N12 (DEC), P413-421

ISSN: 0168-9525

Language: ENGLISH Document Type: REVIEW

Abstract: Site-specific recombinases, from bacteriophage and yeasts have been developed as novel tools for manipulating DNA both in the test-tube and in living organisms. We discuss the characteristics of these enzyme systems, review their application in genetic and developmental studies and speculate on their future potential for large-scale directed modifications of eukaryotic genomes.

2/7/2 (Item 2 from file: 434)

12101712 Genuine Article#: KM161 Number of References: 24

Title: LIGATION OF SYNTHETIC ACTIVATED DNA SUBSTRATES BY SITE-SPECIFIC RECOMBINASES AND TOPOISOMERASE-I

Author(s): PAN GH; LUETKE K; JUBY CD; BROUSSEAU R; SADOWSKI P Corporate Source: UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/; UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO

M5S1A8/ONTARIO/CANADA/; NATL RES COUNCIL CANADA, BIOTECHNOL RES INST, GENET ENGN SECT/MONTREAL H4P 2R2/QUEBEC/CANADA/

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1993, V268, N5 (FEB 15), P 3683-3689

ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE

Abstract: The FLP protein of the 2-mum plasmid of Saccharomyces cerevisiae is a conservative site-specific recombinase that is involved in the amplification of the plasmid. This recombination reaction proceeds via the covalent attachment of the protein to the 3'-phosphoryl group at the site of the breaks through a phosphotyrosine linkage. We have recently developed an assay that measures FLP-mediated strand ligation independent of FLP-mediated cleavage and covalent attachment to the DNA. The substrate for ligation was produced by FLP-induced cleavage of the FLP recognition site followed by digestion with Pronase and was shown to contain (at least) a tyrosine residue at the 3'-PO4 terminus adjacent to the FLP cleavage sites.

We have now synthesized artificial substrates that bear a tyrosine residue on the 3'-PO4 of an appropriate oligonucleotide and find that this substrate is ligated as efficiently as the previous ligation substrates that were isolated after FLP cleavage of the substrate. Analogous substrates for other members of the integrase family of recombinases (lambda integrase protein, P1-Cre protein) as well as for mammalian topoisomerase I are also active as ligation substrates with their cognate protein. This class of activated substrates should be

2/7/3 (Item 3 from file: 434)

11338662 Genuine Article#: HB304 Number of References: 21

Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY

CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM

Author(s): BAYLEY CC; MORGAN M; DALE EC; OW DW

Corporate Source: USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY,DEPT PLANT PATHOL/BERKELEY//CA/94720

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361

Language: ENGLISH Document Type: ARTICLE

Abstract: The Cre-lox site-specific recombination system of bacteriophage P1 was used to excise a firefly luciferase (luc) gene which had previously been incorporated into the tobacco genome. The excision event was due to site-specific DNA recombination between two lox sequences flanking the luc gene and was catalyzed by the Cre recombinase introduced by cross-fertilization. Recombination resulted in the fusion of a promoter with a distally located hygromycin phosphotransferase (hpt) coding sequence and the excision event was monitored as a phenotypic change from expression of luc to expression of hpt. The efficiency of recombination was estimated from the exchange of gene activity and confirmed by molecular analysis. The relevance to potential applications of site-specific deletion-fusion events for chromosome engineering are discussed.

2/7/4 (Item 4 from file: 434)

10707719 Genuine Article#: FB733 Number of References: 25

Title: RECOMBINASE-MEDIATED GENE ACTIVATION AND SITE-SPECIFIC INTEGRATION

TEORNION

IN MAMMALIAN-CELLS

Author(s): OGORMAN S; FOX DT; WAHL GM

Corporate Source: SALK INST BIOL STUDIES, GENE EXPRESS LAB/LA

JOLLA//CA/92037

Journal: SCIENCE, 1991, V251, N4999, P1351-1355

Language: ENGLISH Document Type: ARTICLE

Abstract: A binary system for gene activation and site-specific integration, based on the conditional recombination of transfected sequences mediated by the FLP recombinase from yeast, was implemented in mammalian cells. In several cell lines, FLP rapidly and precisely recombined copies of its specific target sequence to activate an otherwise silent beta-galactosidase reporter gene. Clones of marked cells were generated by excisional recombination within a chromosomally integrated copy of the silent reporter. By the reverse reaction, integration of transfected DNA was targeted to a specific chromosomal site. The results suggest that FLP could be used to mosaically activate or inactivate transgenes for analysis of vertebrate development, and to efficiently integrate transfected DNA at predetermined chromosomal locations.

2/7/5 (Item 5 from file: 434)

10161463 Genuine Article#: DE904 Number of References: 75

RNA IN

NEUROSPORA MITOCHONDRIA Author(s): SAVILLE BJ; COLLINS RA

Corporate Source: UNIV TORONTO, DEPT BOT/TORONTO M5S

3B2/ONTARIO/CANADA/;

UNIV TORONTO, CTR PLANT BIOTECHNOL/TORONTO M5S

3B2/ONTARIO/CANADA/

Journal: CELL, 1990, V61, N4, P685-696

Language: ENGLISH Document Type: ARTICLE

2/7/6 (Item 1 from file: 357)

142790 DBA Accession No.: 93-00842

Gene transfer - gene transmission by retro virus vector, yeast artificial chromosome, mouse zygote homologous recombination, Cre-recombinase method and Flp system (conference abstract)

AUTHOR: Wagner E F

CORPORATE SOURCE: Research Institute of Molecular Pathology (IMP), Dr Bohr-Gasse 7, A-1030, Vienna, Austria.

JOURNAL: Science (258, Suppl., 31-32) 1992 CODEN: SCIEAS

LANGUAGE: English

ABSTRACT: Applications and limitations of gene transfer techniques were discussed. The high efficiency of retro virus infection allows the introduction of genes into cells, e.g. hematopoietic cells. These viral systems provide a method for the generation of animal models for human blood diseases and for possible gene therapy applications. However, the use of yeast artificial chromosomes introduced into cells via DNA-lipid micelles, or the generation of large transgenes through homologous recombination in mouse zygotes, provide a much superior gene transfer system to viral vector systems. Gene transfer techniques are also being used to inactivate a given gene locus by gene targeting. Two new loss-of-function approaches have recently been developed: (1) using the Cre- recombinase; and (2) using the Flp system. These 2 new methods may allow tissue-specific and developmentally regulated gene inactivation in transgenic mice as a function of the site-specific recombinase action. (7 ref)

2/7/7 (Item 2 from file: 357)

141482 DBA Accession No.: 92-13974 PATENT

FLP-mediated gene modification in mammalian cell - vector with FLP-recombinase gene and recombination site for e.g. gene targeting,

gene therapy or transgenic animal development research

PATENT ASSIGNEE: Salk-Inst.Biol.Stud. 1992

PATENT NUMBER: WO 9215694 PATENT DATE: 920917 WPI ACCESSION NO.: 92-331739 (9240)

PRIORITY APPLIC. NO.: US 666252 APPLIC. DATE: 910308

NATIONAL APPLIC. NO.: WO 92US1899 APPLIC. DATE: 920306

LANGUAGE: English

ABSTRACT: A new mammalian recombination system comprises Saccharomyces cerevisiae FLP-recombinase (or a gene encoding it) and DNA containing at least 1 FLP recombination target site. The following are also new:

DNA containing at least 1 FLP recombination site, at least 1 restriction site, at least 1 selectable marker, a bacterial (and optionally a mammal or virus) replication origin; the new DNA inserted

into the FLP recombination target site, and with a 2nd FLP target site in tandem with the 1st; methods for assembly of functional genes for activation of expression in mammal cells, disrupting gene expression in a mammal cells, recovery of transfected DNA from the genome of a transfected organism, and precisely targeted integration of DNA into the genome of a host, all using FLP-recombinase; a transgenic non-human mammal containing at least 1 FLP recombination site in its genome; a method for analysis of mammal development, using the above transgenic mammal and a vector encoding FLP under the control of a conditional promoter, and a reporter gene. The system may also be useful in gene therapy. (49pp)

2/7/8 (Item 3 from file: 357)

089171 DBA Accession No.: 89-07162

Production and isolation of large quantities of monoclonal antibody using serum-free medium and fast protein liquid chromatography - hybridoma cell culture

AUTHOR: Stocks S J; +Brooks D E

CORPORATE SOURCE: Department of Pathology, 2211 Wesbrook Mall, Vancouver, V6T 1W5, Canada.

JOURNAL: Hybridoma (8, 2, 241-47) 1989 CODEN: HYBRDY

LANGUAGE: English

ABSTRACT: A method for the production and purification of monoclonal antibody (MAb) on a large scale is described. 2 Hybridoma lines were used to generate monoclonal antibodies in serum-free medium; a rat-rat hybridoma specific for a surface antigen of a hybrid mouse cell line, and a mouse-mouse hybridoma line specific for rat IgG2a. The serum free medium (RPM1-1640) was supplemented with 5 ug/ml cattle insulin, and incubation was at 37 deg. Both hybridoma lines became confluent within 10 days at maximum cell density. Large-quantities of MAbs were produced in the medium, and purification was easily accomplished within a working day at 4 deg to retain high MAb activity. Ammonium sulfate precipitation, which can cause activity loss, was avoided. The serum free medium was purified by ultrafiltration through an Amicon XM100A filter and fast protein liquid chromatography on a mono Q column with an ionic strength and pH elution gradient. Yields obtained were between 10-30 mg pure MAb/l. (13 ref)

2/7/9 (Item 1 from file: 149)

10844741 Dialog File 149: Health Periodicals Database

Use Format 9 for FULL TEXT

TITLE: Site-specific recombination between homologous chromosomes in Drosophila.

AUTHOR: Golic, Kent G.

JOURNAL: Science VOL.: v252 ISSUE: n5008 PAGINATION: p958(4)

PUBLICATION DATE: May 17, 1991

AVAILABILITY: FULL TEXT Online LINE COUNT: 00224

SOURCE FILE: MI File 47

2/7/10 (Item 1 from file: 399)

118074746 CA: 118(9)74746z PATENT

Site-specific integration and excision of transforming DNA in animal cells using the Flp recombinase of yeast

INVENTOR(AUTHOR): Wahl, Geoffrey M.; O'Gorman, Stephen V.

LOCATION: USA ASSIGNEE: Salk Institute for Biological Studies PATENT: PCT International; WO 9215694 A1 DATE: 920917 APPLICATION: WO 92US1899 (920306) *US 666252 (910308) PAGES: 54 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/85A; C12N-005/16B; C07H-015/12B DESIGNATED COUNTRIES: CA; JP DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; MC; NL; SE SECTION: CA203001 Biochemical Genetics IDENTIFIERS: recombination transforming DNA flp recombinase **DESCRIPTORS:** Development, mammalian... anal. of, developmental regulation of reporter genes in, recombination of transforming DNA using flp recombinase in relation to Genetic element, promoter... developmentally regulated, expression of reporter genes from, recombination of transforming DNA using flp recombinase in relation to Animal cell line, CV-1... Animal cell line, F9... Animal cell line, 293... expression in, of gene for flp recombinase, site-specific recombination of transforming DNA in relation to Enzymes, DNA-recombining... flp, gene for, expression in animal cells of, for site-specific integration or excision of transforming DNA Saccharomyces cerevisiae... Saccharomyces... flp recombinase of, gene for, expression in animal cells of, for site-specific integration or excision of transforming DNA Gene.microbial... for flp recombinase, expression in animal cell culture of, for site-specific integration or excision of transforming DNA Genetic element... frt (flp recombinase target site), site-specific recombination of transforming DNA in animal cells via, expression of flp recombinase gene in relation to Animal cell... mammalian, site-specific recombination of transforming DNA in, flp recombinase and frt sites in Deoxyribonucleic acid sequences... of flp recombinase gene of Saccharomyces cerevisiae Protein sequences... of flp recombinase of Saccharomyces cerevisiae Recombination, genetic, site-specific... Recombination, genetic,

site-specific excisive...

of transforming DNA in animal cell culture, flp recombinase and frt sites in

Mammal...

transgenic, site-specific recombination of transforming DNA in, flp recombinase and frt sites in

CAS REGISTRY NUMBERS:

145752-47-2 amino acid sequence of, complete, and expression in animal cell culture of gene for

145752-45-0 nucleotide sequence of

145752-46-1 nucleotide sequence of, complete, and expression in animal cell culture of

145752-44-9 nucleotide sequence of, in transforming DNA for site-specific recombination of transforming DNA

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2/7/11 (Item 1 from file: 265)
0103231 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS
IDENTIFYING NO.: 1R01HD30255-01 AGENCY CODE: CRISP
FATE MAPS OF EMBRYONIC GENE EXPRESSION IN MICE
PRINCIPAL INVESTIGATOR: O'GORMAN, STEPHEN V
ADDRESS: SALK INSTITUTE PO BOX 85800 SAN DIEGO, CA 92186-5800
PERFORMING ORG.: SALK INSTITUTE FOR BIOLOGICAL STUDIES, SAN DIEGO.

CALIFORNIA

SPONSORING ORG.: NATIONAL INSTITUTE OF CHILD HEALTH AND HUMAN DEVELOPMENT

FY: 93 FUNDS: \$260,269 TYPE OF AWARD: New Award (Type 1) SUMMARY: The long term objective of the research initiated by this proposal is to investigate the genetic regulation of mammalian development. The principal experimental objective is to compile fate maps of the mature fates of cells that descend from progenitors that transiently express specific candidate mammalian developmental control genes during embryonic and fetal stages in transgenic mice. This will be done both in normal mice, and in mice that fail to express the normal products of genes of interest. A novel molecular paradigm for fate mapping will be employed that is based on the precise recombination of transgenes by the yeast recombinase FLP. By this means, the transient activity of a gene can be used to indelibly mark not only the cells in which the gene is expressed, but all of its descendants, even if the latter do not express the gene.

The specific aims of this proposal are to define the descendant domains (lineages) established by progenitors that transiently express Hox 2.9. Krox 20, or Hox 2.6 in the hindbrain and adjacent branchial arch tissues in both normal animals and in, animals that fail to express the normal products of these genes. Both the descendant expression domains and the descendant functional domains of these genes will be mapped and distinguished from one another. The first product of the research program will be a fate map of the mouse that correlates early patterns of gene expression with the organization of cells and tissues in the mature, normal animal. The second product will be a knowledge of whether, and if so how, these fates are altered when the gene of interest is not expressed. They will additionally address the question of compartmentation in the mammalian hindbrain and branchial arches. The maps of normal and mutant cell fates will enormously increase our understanding of the roles played by individual genes in the intricate genetic program that regulates mammalian development, and additionally provide a wealth of new information about cell proliferation, cell mixing, and cell migration in the mammalian embryo. In this manner, the research program will contribute to an improved understanding of normal mammalian development and to the kinds of developmental deficits that arise from alterations in specific gene products.

2/7/12 (Item 1 from file: 286) 0050984 Journal Announcement: 08APR91 Doc Type: 2 Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355

PRIORITY DATE (DEMAND FOR INTERNATIONAL APPL. FILED PRIOR TO EXPIRATION OF 19TH MONTH FROM PRIORITY DATE)

No of Legal Status: 006

2/7/15 (Item 1 from file: 351)

009204307 WPI Acc No: 92-331739/40

XRAM Acc No: C92-147538

FLP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development

Patent Assignee: (SALK) SALK INST BIOLOGICAL STUDIES

Author (Inventor): OGORMAN S V; WAHL G M

Number of Patents: 001 Number of Countries: 016

Patent Family:

CC Number Kind Date Week

WO 9215694 A1 920917 9240 (Basic)

Priority Data (CC No Date): US 666252 (910308) Applications (CC,No,Date): WO 92US1899 (920306)

Language: English

EP and/or WO Cited Patents: 10Jnl.Ref; US 4959317; US 4997757

Designated States (National): CA; JP

(Regional): AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; MC; NL; SE

Abstract (Basic): WO 9215694 A

Mammalian recombination system (I) comprises:- (a) FLP recombinase or a nucleotide sequence encoding it, and (b) a first DNA comprising a nucleotide sequence contg. up to 1 FLP recombination target site.

Also new are:- (1) a DNA construct comprising as an autonomous fragment, up to 1 FLP recombination target site, up to 1 restriction endonuclease recognition site, up to 1 marker gene, a bacterial origin of replication and opt. a mammalian cellular or viral origin of replication; (2) a DNA construct like that of (1) where the components are contained as an insert in the FLP recombination target site and a 2nd FLP target site is in tandem with the first; (3) assembling of functional gene(s) which is (are) suitable for activation of expression is mammalian cells. The gene segments, derived from up to 1 gene, are individually inactive but contain up to 1 recombination site and are assembled into a functional DNA by contacting with FLP recombinase; (4) disrupting functional gene expression in mammalian cells. Gene of interest contains up to 1 FLP recombination site and is contacted with FLP recombinase and a DNA segment also contg. up to 1 FLP site; (5) the recovery of transfected DNA from the genome of a transfected organism. The DNA contains a fragment with 2 tandemly oriented FLP recombination sites and is contacted with FLP; (6) precisely targeted integration of DNA into the genome of a host organism. An FLP recombination site is introduced into the genome of compatible cells, DNA contg. a recombination site is integrated using FLP recombinase and transformed cells are then introduced into the subject; (7) a mammalian cell contg. up to 1 FLP recombination site in its geromic DNA; (8) a transgenic, non-human mammal contg. up to 1 FLP recombination site in its genome. (9) analysis of the development of a

Salk Institute scientists have shown that the site specific recombinase enzyme, FLP, from Saccharomyces cerevisiae can be used for gene activation in mammalian cells and have suggested it may be useful to mosaically inactivate or activate transgenes or to efficiently integrate transfected DNA at predetermined chromosomal locations.

2/7/13 (Item 1 from file: 315)

328071 CÈABA Accession No.: 24-12-020674 DOCUMENT TYPE: Patent Title: FLP-mediated gene modification in mammalian cells, and compositions and cells useful therefor.

AUTHOR: Wahl, G. M.; O'Gorman, S. V.

CORPORATE SOURCE: Salk Inst. Biol. StudiesLa Jolla, CA 92037USA

CODEN: PIXXD2

PATENT NUMBER: WO 9215694

PUBLICATION DATE: 17 Sep 1992 (920917) LANGUAGE: English PRIORITY PATENT APPLICATION(S) & DATE(S): US 666252 (910308)

ABSTRACT: A gene activation/inactivation and site specific integration system which was developed for mammalian cells is disclosed. The system is based on the recombination of transfected sequences by FLP, a recombinase derived from Saccharomyces. FLP was shown to rapidly and precisely recombine copies of its specific target sequence in several cell lines e.g. a chromosomally integrated, silent .beta.-galactosidase reporter gene was activated for expression by FLP-mediated removal of intervening sequences to generate clones of marked cells whilst, the reverse reaction, is used to target transfected DNA to specific chromosomal sites. FLP can therefore mosaically activate or inactivate transgenes for a variety of therapeutic purposes, as well as for analysis of vertebrate development.

2/7/14 (Item 1 from file: 345) 11153531

Legal Status (No, Type, Date, Code, Text)

WO 9215694 P 910308 WO AA PRIORITY (PATENT) US 666252 A, 910308

WO 9215694 P 920306 WO AE APPLICATION DATA (APPL. DATA) WO 92US1899 A 920306

WO 9215694 P 920917 WO AK DESIGNATED STATES CITED IN A PUBLISHED APPLICATION WITH SEARCH REPORT (DESIGNATED STATES CITED IN A PUBLISHED APPL. WITH SEARCH REPORT)
CA JP

WO 9215694 P 920917 WO AL DESIGNATED COUNTRIES FOR REGIONAL PATENTS CITED IN A PUBLISHED APPLICATION WITH SEARCH REPORT (DESIGNATED COUNTRIES FOR REGIONAL PATENTS CITED IN A PUBLISHED APPL. WITH SEARCH REPORT)

AT BE CH DE DK ES FR GB GR IT LU MC NL SE

WO 9215694 P 920917 WO A1 PUBLICATION OF THE INTERNATIONAL APPLICATION WITH THE INTERNATIONAL SEARCH REPORT (PUB. OF THE INTERNATIONAL APPL. WITH THE INTERNATIONAL SEARCH REPORT)

WO 9215694 P 921223 WO DFPE DEMAND FOR INTERNATIONAL APPLICATION

FILED PRIOR TO EXPIRATION OF 19TH MONTH FROM

mammal comprising:- (a) providing a transgenic mammal comprising:- (i) an expression construct encoding FLP under the control of a condition promoter; and; (ii) a reporter construct under the control of the same or a different promoter. The reporter construct encodes a functional or non-functional gene contg. a recombination site such that functional expression is disrupted or functional expression commences on FLP recombination; and (b) following the development of the mammal to determine when expression of functional reporter gene product either commences or is disrupted; and (10) as co-transfection assay for the occurrence of FLP-mediated recombination in which the expression construct and reporter construct outlined above are contained within plasmids in a mammalian cell.

USE/ADVANTAGE - (I) allows selective modification of chromosomal or extrachromosomal DNA in mammalian cells. Inheritance of genetic sequences and the fate of genetic sequences during development can be studied in a wide variety of tissues in different organisms. Simple histochemical assays can be used for analysis Dwg.0/3B

Derwent Class: B04; C06; D16;

Int Pat Class: C07H-015/12; C12N-005/16; C12N-015/85

2/7/16 (Item 1 from file: 624)

0432248 DIALOG File 624: McGraw-Hill Publications Online

FLP-mediated gene modification in mammalian cells, and compositions and cells useful therefor

Biotechnology Newswatch November 16, 1992; Pg 9; Vol. 12, No. 22

Journal Code: BIO ISSN: 0275-3687

Section Heading: Biotechnology PatentWatch

Word Count: 143

TEXT:

WO 92/15694

Published: Sept. 17, 1992

Filed: March 6, 1992 Priority: March 8, 1991

The Salk Institute For Biological Studies, La Jolla, Ca

A gene activation/inactivation and site-specific integration system has been developed for mammalian cells. The invention system is based on the recombination of transfected sequences by FLP, a recombinase derived from Saccharomyces. In several cell lines, FLP has been shown to rapidly and precisely recombine copies of its specific target sequence. For example, a chromosomally integrated, silent b- galactosidase reporter gene was activated for expression by FLP-mediated removal of intervening sequences to generate clones of marked cells. Alternatively, the reverse reaction can be used to target transfected DNA to specific chromosomal sites. These results demonstrate that FLP can be used, for example, to mosaically activate or inactivate transgenes for a variety of therapeutic purposes, as well as for analysis of vertebrate development.

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Number of sequences searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IntelliGenetics
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k 79, all MAMMALIAN entries

k 79, all OTHER MAMMALIAN entries

k 79, all OTHER VERTEBRATE entries

k 79, all PATENT entries

k 79, all PRIMATE entries
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1 OTHER VERTEBRATE entries
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112413
4909
                                                                                                                                                                                                                                                                                                                                                                                                                                        SCORE 0
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Number of sequences
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Gap penalty
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f raised to 8.
f raised to 10.
f raised to 11.
raised to 12.
raised to 13.
raised to 14.
raised to 15.
                                                                                                                     sequences searched: scores above cutoff:
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Joining penalty
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≤⊴≈ពេលពេលពេល		Results of Data bank : El Data bank : El Data bank : El	y sequence b er of sequen	6. MUSHKPRO 7. S56291 8. HSFGL2 9. MUSHFR3 0. HUMPOMM	5. Q29100	Sequence Name	The list of other	1. Q25185 2. Q44265 3. Q12154 4. 2MICRON-B	Sequence Name	100% similar se	Cut-pff raised to The scores below a Significance is ca
79, all PATENT entries 79, all PRIMATE entries 79, all RODENT entries 79, all RODENT entries 79, all RODENT entries 79, all OTHER MAMMALI NEW 11, all OTHER VERTEBH- NEW 11, all PRIMATE entries 67, all entries 679, all entries 679, all entries 679, all entries	11, all RODENT entries 79, all MAMMALIAN entries 79, all OTHER MAMMALIAN e 79, all OTHER VERTEBRATE	f the optimized comparison of FLP1 (1-34 EMBL-NEW 11, all MAMMALIAN entries EMBL-NEW 11, all OTHER MAMMALIAN entries EMBL-NEW 11, all PRIMATE entries	Ouery sequence being compared: FLP1 (1-34) Number of sequences optimized: 4909	Mouse house-keeping protein m sam3=FGFR3 homolog (mice, bra Human F1g-2 gene for fibroblas BALB/c fibroblast growth fact Human 35kD peroxisomal membra	**** 5 standard deviations above mean Sequence of FLP recombination 33 **** 3 standard deviations above mean	Description	r best scores is:	pSW6 expression vector. pSW6 for expression of LD78 s Shuttle vector pSW6. B form of the yeast 2micron p	 	sequences to the query sequence were	Cut-pff raised to 17. The scores below are sorted by initial score. Significance is calculated based on initial score.
entries	ntries entries	(1-34) with:		2415 23 2520 23 2887 23 4158 23 1523 22	ove mean **** 33 33	Init.		7984 34 7859 34 7859 34 6248 34	Init. Op Length Score Sc	found:	
				24 23 23 3 23 3 3 3 3	33 5	Opt. Score Sig.		34 34 6 6	Opt. Score Sig.	-	
				3.50 3.50 3.50 3.50 3.50 3.27	.83 0	g. Frame		6.06 6.06 0	g. Frame		
Gap penalty Gap size penalty Cutoff score Cutoff score Randomization group Initial scores to soptimized scores to Optimized scores to Number of residues: Number of sequences	Similarity matrix Mismatch penalty	STDEV-3 SCORE15	0	ى (ا	10-	1 1 1) I	\$ 100- - 50-	e O Z I	77 CD FC	F 1000 -
an de	matrix enalty	16	-				*			,	
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ndomizations 1 o save 10 ext 0 Standard Deviation 1.23 Total Elapsed 00:04:10.00		22	-					1 *	-		
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The acores below are sorted by optimized score. Significance is calculated based on optimized s based on optimized score

4 100% similar sequences to the query sequence were found:

			Init. Op				
Sequence Name		Length	Length Score Score Sig. Frame	ore	Sig. Fi	came	
1. 025185	1. 025185 psw6 expression vector.	7984	7984 34 34 13.06 0	34	13.06	0	
2. 044265	pSW6 for expression of LD78	•	34	34	34 13.06	0	
3. 012154	Shuttle vector pSW6.		34	34	13.06	0	
4. 2MICRON-B	B form of the yeast 2micron p	p 6248	34	34	13.06	0	
The list of other best scores is:	best scores is:						

Sequence Name	Description	Init. Opt. Length Score Score Sig. Frame	Init. Opt. Score Scor	t. ore	Sig. Fr	ame.
	**** 12 standard deviations above mean ****	bove mean) + > + + *	,		>
5. Q29100	**** 5 etandard deviations above mean ***	33 hove mean	*ω *ω *	33	33 12.24	0
	Standard deviations above mean	ure wear		n n	n 1	>
RSCALPST	Rat mRNA for calpastatin	1931	18	25	5.71	c
RABCALPA	Rabbit calpastatin mRNA, comp 3689		22	25	5.71	0
	**** 4 standard deviations above mean ****	bove mean	* * *			
8. MUSHKPRO	Mouse house-keeping protein m	2415	23	24	4.90	0
9. HUMPC101	Human plasma cell membrane gl	3486	16	24	4.90	0
10. Q39050	K.lactīs/S. cerevisae genetic	6824	19	24	4.90	0
1. FLP1 (1-34)	news everyosesion ventor					

COTON pswb expression vector

CCCCCCCCS THE TRANSPORT OF THE TRANSPORT Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10; phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss. Q25185 standard; DNA; 7984 BP. Saccharomyces cerevisae. pSW6 expression vector. 18-NOV-1992 (first entry)

23-OCT-1991; G01860. 24-OCT-1990; GB-023149.

New proteins comprising active protein and integrin-affinity sequence - are antithrombotics useful in treating and preventing myocardial infarction, stroke, pulmonary embolism and deep vein (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Dawson KM, Edwards RM, Fallon A; WPI; 92-183627/22.

Disclosure; Page 67; 101pp; English. thrombosis

The sequence given is the yeast expression vector pSW6. It is based on the 2 micron circle from Saccharomyces cerevisae. It is a shuttle vector capable of replication in both S. cerevisae and Escherichia coli as it contains the origin of replication for both organisms. It also contains the leu2 gene (a yeast selectable marker) and the amipicillin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced ability for passage through E.coli and this greatly facilitates genetic manipulation with this vector. pSW6

Residue Identity 8888888888888 epidermal growth factor (EGF). The expression of the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSW6 can be removed by digestion with HindIII and BamMI. This removes DNA encoding both EGF and S amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSW6 the alpha-factor pro-peptide. the alpha-factor pro-peptide. Genes to be inserted into the pSW6 expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BanHI site.

Sequence 7984 BP; 2348 A; 1698 C; 1635 G; 2303 T; contains contains an alpha- factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under 0 0 U 34 100% 0 Optimized Score = 34 Matches = 34 Conservative Substitutions 34 34 Mismatches Significance = 13.06 0 0

FLP1 (1-34) Q44265 Q44265 standard; DNA; 7859 BP. pSW6 for expression of LD78 synthetic gene

misc_difference 1773 Saccharomyces cerevisiae. SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha; macrophage inflammatory protein; multimer; tumour therapy; 23-NOV-1993 (first entry) pSW6 for expression of LD78 synthetic gene. psoriasis; hyperproliferation; yeast expression vector; /note= "base illegible in the specification" Location/Qualifiers

WO9313206-A.

3-DEC-1992; G02390.

23-DEC-1991, GB-027319. 14-OCT-1992; GB-021587. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Craig S, Czaplewski LG, Edwards RM, Gilbert

WPI; 93-227322/28.

Protein with stem cell inhibition activity, e.g. LD78 or M1P-1 alpha - unable to form stable multimer higher than dodecamer,

The secretion signals from the yeast mating type factor alpha were used to direct export of the LD78 protein. The yeast expression vector pSW6 (NCIMB 40326) is based on the 2 micron circle from providing better tissue penetration Disclosure; Page 159-168; 294pp; English. An expression vector was designed to enable secretion of LD78 the extracellular medium after expression in S. cerevisiae. Secretion aids purification and rapid analysis of LD78 ç

S. cerevisiae 7859 BP; 2317 A; 1667 C; 1585 G; 2289 T;

Gaps

Residue Identity Initial Score SQ () 1 Others;

34 100% 0

Optimized Score Matches Conservative

34

Significance Mismatches

= 13. .06

Substitutions a n

124

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3. FLP1 (1-34)
Q12154
               this fusion is under control of a galactodse regulated promoter this fusion is under control of a galactodse regulated promoter and which contains bybrid DNA from S. cerevisiae GAL 1-10 promoter and the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF gene can be exclsed by digestion with HindIII and BamHI. The plasmid was used for the expression of a synthetic hirudin HV-1 gene in E. coli K12 HW87. The plasmid can be used to construct expression vectors in which the hirudin gene is linked to a second gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide link contains a cleavage site for e.g. factor X or thrombin which can be cleaved, releasing the individual proteins which have anti-thrombotic activity. The enzymes which cleave the fusion protein are present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 71; 115pp; English.

The vector is based on the 2u circle from S. cerevisiae. It is deposited in S. cerevisiae strain bJ2168 as NCIMB 40326. It is a shuttle vector capable of repication in both E. coli and S. cerevisiae and contains origins of replication for both, the leu2 gene (selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli ColEI-based replicon pATI53. The vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of the factor is made and the sequence of the sequences are derived from E. coli colEI-based replicon pATI53. The vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1989;
07-DEC-1990;
occurring.
See also Q12153-Q12156, Q12158-Q12162 and Q12490.
Sequence 7859 BP; 2317 A; 1656 C; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRBI-) BRIT BIO-TECHN LTD.
Dawson KM, Hunter MG, Czapleswski LG;
WPI; 91-208151/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1990; G01911.
07-DEC-1989; GB-027722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein; blood clotting; coagulation; fibrinolysis;
antithrombotic; thrombolysis; streptokinase; plasmid; circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q12154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q12154 standard; DNA; 7859 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shuttle vector pSW6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                     <u>و</u>;
                     2286 T
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residue
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        Residue Identity
                                                   FLP1 (1-34)
2MICRON-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FLP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the A form in Genbank. Not available commercially. No antibiotic
                                                                                                                                                               pept
                                                                                                                                                                                                                                                                                                                                             Broach J.R.;
"The yeast plasmid 2u circle";
Cell 28: 203-204 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                     B form of the yeast 2micron plasmid
                                       Sequence 6248
                                                                                                repeat_unit
                                                                                                                                           pept
                                                                                                                                                                                                                                                                                                                                                                                                 Vector; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-1986
                                                                               repeat_unit
                                                                                                                                                                                                           resistance or color markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2MICRON-B
                                                                                                                                                                                                 (SUPPLIER (NONE COMMERCIAL))
                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                          /note="REP1"
4308..5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
                                                                                                                          5570..6319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 6248 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H II A
  0 (0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       form of the yeast 2micron plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
100%
0
34
100%
0
                                      /note="2 micron replicon"
BP; 1961 A; 1188 C; 1248 G;
                                                                                /note="inverted repeat"
3714..4112
                                                                                                      341..938
                                                            /note="inverted repeat" 700..1050
                                                                                                                                                                   3769..2644
                                                                                                                                                                                       Location/Qualifiers
                                                                                                             /note="FLP"
                                                                                                                                  /note="REP2"
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          Optimized Score Matches
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4
           Mismatches
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Mismatches
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Conservative Substitutions

d.

29-MAY-1991

7-3-1 HONGO,

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Initial Score = 33
Residue Identity = 100%
Gaps = 0
                              6
                                                                                                                                                                                                                                                                          rransgenes for therapeutic purposes and analysis of development transgenes for therapeutic purposes and analysis of development Claim 33; Page 40; 49pp; English.

FIP recombinates is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy number of the 2-mu plasmid of S. cerevisiae during DNA replication. The inventors claim a mammalian recombination system in which the FIP recombinates is pref. 029101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair spacer (see Q29100). The nucleotides in the spacer region can be replaced with any other combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of the FRT has only 12 base pairs on the 3' end of the spacer. The apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; 6 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLP1 (1-34)
Q29100
                            FLP1 (1-34)
             RSCALPST
                                                                                WPI; 92-331739/40.

FLP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1992; U01899.
08-MAR-1991; US-666252.
(SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of FLP recombination target site FLP recombinase; site-specific integration system; gene activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogorman SV, Wahl GM; WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene inactivation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       029100;
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           Rat mRNA for calpastatin
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                                                                                                                                                                                                                   Optimized Score Matches
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                                                                                                                                                                                                                     33 Significant
33 Mismatches
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                                                                                                                                                                                                     12.24
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                        Initial Score
Residue Identity
                                  7. FLP1 (1-34)
RABCALPA
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STANDARD
FEATURES
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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ORGANISM
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JOURNAL
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X 400 410 420 X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1931)
1 Ishida, S., Emori, Y. and Suzuki, K.
Rat calpastatin has diverged primary sequence from other mammalian calpastatins but retains functionally important sequences
Biochim. Biophys. Acta 1088, 436-438 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp. Rattus sp. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 1931)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full automatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-NOV-1990) Y. Emori, DEPT OF BIOPHYSICS & BIOCHEMISTRY, FACULTY OF SCIENCE, UNIVERSITY OF TOKYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calpastatin; CANP inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat mRNA for calpastatin X56729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSCALPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full automatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUNKYO-KU, TOKYO 113, JAPAN
                                  Rabbit calpastatin mRNA,
                                                                                                                                                                                                                            B 0 0
                                                                                                                                                                                                                                                                                                                   671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
                                                                                                                                                                                                                          18
77%
2
                                                                                                                                                                                                                                                                                                                                      EAEEQLPPLSDDFLLDALSQDFSSPANILSLGFEDAKLSAAVSETVSQVPAPSNHTAA
PPPGTERRDKELDDALDELSDS1GQRQPDFDENKFLDDKVKEKLKAEHSEKLGERDDT
IPPEXTRHLLNDGKDKEKEKPLDKEHREAGQDQDPIDALSEDLDSCPPTTETSQNTTKE
KGKKTSSSKASKNEEKTKDSSKKTEEVPKPKVDEDAT*
                                                                                                                                                                                                                                                                                                                                                                                                           PPYTGPVVLDPMDSTYLEALGIKEGTIPPEYRKLLEKNEAITGPLPDSPKPMGIDHAI
DALSSDFTCSSPTGKQTEKEKSTGESSKAQSAGVTRSAVPPQEKKRKVEEEVMNDQAL
QALSDSLGTRQPDPQSHLRQAKQVKEAKAKEEERQEKGGEDEDTVPAEYRLKPAKDXDG
KPLLPEPEETSKCLSESELIGELSADFVQPTYQEKPSKPAKIKKGVVPDDAVETLAR
SLGTRKEDPEDEKSIJDKVKEKAKEEDHEKLGEKEETIPPDYRALIKKGVVPDDAVETLAR
SLGTRKEDPEDEKSIJDKVKEKAKEEDHEKLGEKEETIPPDYRALIKKGVVPDDAVETLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSTTGAKPPVIHEKKPKGKPKEGSETKFQDAPSADGESVAGDVT
VATASDEVVVKKKEKKSLTPTLPMESTLNKLSDKSGVNAALDDLIDTLGECEDTNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus sp."
/tissue_type="liver"
/clone_lib="cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="calpastatin/CANP inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="calpastatin/CANP inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evidence=EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                       406
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                                                                                                                                                                                                                                                                                                                 463 g
                                    complete cds.
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27
3
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Locus

RABCALPA

3689 bp ss-mRNA

15-JUN-1989

5.71 6 0

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Gaps
                                                                                     8. FLP1 (1-34)
                                                                                                                                                                                                                                                                                                  Initial Score
Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
DEFINITION Mouse house-keeping protein mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS Emori,Y., Kawasaki,H., Imajoh,S., Imahori,K. and Suzuki,K. RFTIE And Endogenous inhibitor for calcium-dependent cysteine protease contains four internal repeats that could be responsible for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                 MUSERPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcium-dependent cysteine protease; calpastatin. Rabbit lung or heart, cDNA to mENA, clones lambda-Cl-[2,311,11,21,213,413,408].
                     MUSHKPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Lagomorpha; Leporidae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit calpastatin mRNA, complete cds.
                                                             Mouse house-keeping protein mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A. 84, 3590-3594 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPEEGKPVADK IKEKSKEEEREKLGEKEETIPPDYRLEEAKDKOKRD LLPSEPTAQLI
ALSEDILLDALSED GOROOPDPEMKEMEDKYKERAKKEHKOKLGERDT IP PEYRH
SNKELDDALDKLSOSLGOROPDPEMKEMEDKYKERAKKEHKOKLGERDT IP PEYRH
LLDQGEQDKPEKPPTKKSKE IKKPAGDQDP IDALSGDLDSCPPAAETSQATEKDKSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQEKKRKVEEDAMSDQALEALSASLGTRMAEPELDLSSIKEVAEAKRKEEKVEKCGED
DETVPAEYRLKPATDKDGKPLLPEPAEKPKPRSESELIDELSKDFSQAKSNEKQPKPT
GKTEESKAAVPAPVAEAVPRTSMCSIQPVPFKPASLQKSTVPDDAVEALAGSLGRKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDHEKKAQEGKPKEHTKPKSTHKHASDGEGKHGRNEKTASRSKEPVTPAKRTEPETKP
QDTKEAGGKSVAAGTTAAPGKAGDPKCEKKSLPAALAEPKPDEPSGKSGMDAALDDL
IDTLGEPSETJCEDSTAYTGPEISDPMSSTYIEELGKREVTLIPFKYRELLEKKTGVAGP
PPDSVTPLGPDDAIDALSSDFTCSSPVASGKEAGKEAAKSAGEVLEALSAKVMRAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429..2313
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryctolagus cuniculus"
930 c 943 g 733 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/note="calpastatin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="calpastatin mRNA"
160..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'codon_start=1
'transTation="MNPAEAKAVPISKEMEGPHPHSKKRHRRQDAKTEPEKSQSTKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="calpastatin precursor; (EC 3.4.22.17)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="calpastatin signal peptide"
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                       2415 bp ss-mRNA
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27
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Mismatches
                       21-AUG-1991
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      9. FLP1 (1-34)
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ORIGIN
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CDS
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AUTHORS
JOURNAL
STANDARD
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SOURCE
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                       FEATURES
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                                               STANDARD
                                                                                                             TITLE
                                                                                                                                                                                                                                         ORGANISM
                                                                   JOURNAL
                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                         Human plasma cell membrane glycoprotein (PC-1) mRNA, complete w57736 J05654
                                                             Plasma cell membrane glycoprotein PC-1: cDNA cloning of the human molecule, amino acid sequence, and chromosomal location J. Biol. Chem. 265, 17506-17511 (1990)
                                                                                                                                                                     Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. 1 (bases 1 to 3486)
                                                                                                                                                                                                                                                                              plasma cell membrane glycoprotein PC-1.
Human placenta, cDNA to mRNA, clones lambda-hPC1-2 and lambda-hPC1-3; Human fetal liver, cDNA to mRNA, clones
                                               full automatic
                                                                                                                                                  Buckley, M.F., Loveland, K.A., McKinstry, W.J., Garson, O.M.
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wang, B., Hunsperger, J.P., Laib, J. and Fan, D.
Unpublished (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (bases 1 to 2415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRVELNMFVSEKEFRKLIATPKRPDLYQVMAVLWQVACDVKFLHMEPWSSFSVHMENG
HLEKSKHGESVNLLKQNLYLVRMTPRRTLFTENLSPLNYDIFFHLVKHCFGKRNAPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transTation="MRGPAMRLPPRLALSALARGPSCILGSGAATRKDWQTRNGRGFS
DFNIEDLEDSDLEESSPWTSRNRSEPTHHIACKAARNILVROLLEDFNEDSRQILLECN
PGRGILTGALLKAGARRVAFESEKTFICHHIACKACRNADGELOVHCOFFKMDFYCGV
VRPDVSSQAIFQNLGIKAVPWSAGVPIKVFGILPYKHERRILMKILFDLYSCESIYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
478 c 535 g 671
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                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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24 Mismatches
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10
0
                                                                                                                                                                                                                                                                                                                                                                       cds.
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mRNA

polyA_signal

/gene="PC1" 3130..3135

.64..2785 'gene="PC1"

gene="PC1"

product="plasma cell membrane glycoprotein PC-1"

'gene="PC1"

```
This sequence represents a genetic vector which allows the stable multiple integration of DNA sequences into the genome of Kluyeromyces lactis and Saccharomyces cerevisiae. This sequence can be used in an
                                                                                                                                                         heterologous proteins
Claim 1; Fig 1; 26pp; English.
                                                                                                                                                                                                                                                        which allows stable multiple integration of DNA for prodn. of
                                                                                                                                                                                                                                                                                                                  Vector for Kluyeromyces lactis and Saccharomyces cerevisiae
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255

KNIKVIYĞPAARLRPSDVPDKYYSFNYEGIARNLSCREPNQHFKPYLKHFLPKRLHFA KSDRLEPLTFYLDPQWQLALMPSERKYGSGFHGSDRNFSNMQALFVGYGPGFKHGIE ADTFENIEVYNLMCDLLNLTPAPNNGTHGSLNHLLKNPVYKHPKEVHPLVQCPFTR NPRDNLGCSCNPSILPIEDFQTQFNLTVAEEK IIKHETLPYGRPRVLQKENTICLLSQ HQFMSGYSQDILMPLMTSYTVDRNDSFSTEDFSNCLYQDFRIPLSPVHKGSFYKNNTK VSYGFLSPPQLNKNSSGIYSEALLTINIVPMYQSFQVIMRYFHDTLLRKYAEEENGVN INGIFPDIYKYYNGSVPFEERILAVLQWLQLPKDERPHFYTLYLEEPDSSGHSYGPVS SEVIKALQRVDGMVGMLMDGLKELNLHRCLNLILISDHGMEQGSCKKYIYLNKYLGDV SDILKLKTHLPTFSQED" VVSGPVFDFDYDGRCDSLENLRQKRRVIRNQEILIPTHFFIVLTSCKDTSQTPLHCEN SHGIIDNKMYDPKMNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFFWPGSDVE GEKRLTRSLCACSDDCKDKGDCCINYSSVCQGEKSWVEEPCESINEPQCPAGFETPPT LLFSLDGFRAEYLHTWGGLLPVISKLKKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPE /transTation="MDVGEEPLEKAARARTAKDPNTYKVLSLVLSVCVLTTILGCIFG LKPSCAKEVKSCKGRCFERTFGNCRCDAACVELGNCCLDYQETCIEPEHIWTCNKFRC LDTLAFILPHRTDNSESCVHGKHDSSWVEELLMLHRARITDVEHITGLSFYQQRKEPV codon start=1

BASE COUNT 1022 /organism≕"Homo sapiens" 720 c 756 g 988

Residue Identity Initial Score H H 16 70% Optimized Score Matches Conservative Substitutions 24 Significance26 Mismatches 4

2520

10. FLP1 (1-34) Q39050 GAATGCTTCCTTTTCACTTAAAAGTAAAGAGAAATTT 860 870 880 890 X

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Q39050 standard; DNA; 6824 BP. Q39050;
K.lactis/S. cerevisae genetic vector.
                           28-JUL-1993 (first entry)
                                                                                                                      K.lactis/S. cerevisae genetic vector.
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21-APR-1993. 31-AUG-1992; 114838. 31-mug-1991; IT-MIZ349. FLP; Genetic; vector; integration; Kluyeromyces lactis; 255 ribosomal DNA; Saccharomyces cerevisiae; E. coli; domain; yeast; plasmid; promoter; expression cassette; HIS3; marker; transformant; human; lysozyme; HIZ; GAL7; signal sequence; killer toxin; transcription termination signal; (ISTS) SCLAVO SPA. EP-537456-A. ; signal sequence; 2 micron plasmid; 88. Rossolini GM, Thaller MC;

Galeotti CL, Gall WPI; 93-127394/16.

Residue Initial Score GAAGTTCCTATTCTCTAGACAG--CCGGACGGTGGCCA X 10 20 30 X GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT----C production and secretion into the culture medium of human lysozyme. This complete transformation vector is 7850 bp long and includes the integration vector of the invention and an expression cassette comprising the K. lactis GAL7 promoter, the signal sequence of the K. lactis killer toxin, the cDNA encoding the ripe form of human lysozyme (HLZ) and the transcription termination signal FLP of the 2 micron plasmid Sequence integration plasmid, such as expression cassettes. The gene HIS3 from K. lactis and S. cerevisiae is pref. used as a genetic marker for the selection of transformants and an expression cassette for the integrating unit consisting of two not contiguous sequences of the 20 ribosomal DNA from S. cerevisiae, flanking a genetic marker suitable for selection of the yeast transformants in which the integration event has occured. Other DNA sequences may be introduced into the integrating vector which comprises a region necessary for the stable maintenance of the plasmid in ${\bf E}.$ coli and a domain which acts as an Score = Identity = = from S. 6824 BP; 19 65% 6 cerevisiae. Conservative Substitutions Optimized Score = Matches = 1815 A; 1521 C; 24 25 1726 G; Significance = Mismatches = 1762 4.90 7 0

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Query sequence being compared:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Results file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                                                                                                                                                                                                         Results of the initial comparison of FLP (1-34) with:
ca bank : EMBL-NEW 11, all MAMMALIAN entries
ca bank : EMBL-NEW 11, all OTHER MAMMALIAN entries
ca bank : EMBL-NEW 11, all PRIMATE entries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                             flp.res\made by low on Tue 1 Feb 94 14:55:48-PST.
                                                                                                                                                                              GenBank 79, all OTHER MAMMALIAN entries GenBank 79, all OTHER MAMMALIAN entries GenBank 79, all OTHER VERTEBRATE entries GenBank 79, all PATENT entries
                                                                                                                                                                     PRIMATE entries
                                                                                                   ODDENT entries
11 OTHER WAMMALIAN entries
11 OTHER VERTEBRATE entries
11 PRIMATE entries
                                                                                     11 RODENT entries
                                                                                                                                                                                                                                                                                                                                                                FLP (1-34)
112413
3751
                                 Similarity matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100-
                   Unitary
1
                                                                     PARAMETERS
                                                                                                                         15
K-tuple
Joining penalty
Window size
                                                                                                                         3<sup>19</sup> –
     304
                                                                                                                                         34
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E 5000-	*	,	F10000-	0	ı	π	(F)	B	3	050000 -	Z	1	100000-	
			*	*	*									

Initial scores to save Optimized scores to save

10

Alignments to save Display context

010

Deviation

Number of randomizations

Gap penalty
Gap size penalty
Cutoff score Mismatch penalty

1.00 0.33 1 1

Randomization group

1000-* 500-

Cut-off raised to 8. Cut-off raised to 9. Cut-off raised to 11. Cut-off raised to 12. Cut-off raised to 13. Cut-off raised to 14. Cut-off raised to 15. Cut-off raised to 15.	Number of residues: 92888128 Number of sequences searched: 112413 Number of scores above cutoff: 3751	Times: CPU Total El 00:05:52.89 00:12:19	Scores: Mean Median Standard 9 10 4.34	SEARCH STATISTICS
		Total Elapsed 00:12:19.00	Standard Devia 4.34	

((() ()	5000		Data bank : VectorBank 6.4, all entries Data bank : VectorBank 6.4, all entries	bank : GenBank-NEW 11, all PRIMATE entries bank : GenBank-NEW 11, all RODENT entries bank : GenBank-NEW 11, all notries	bank : GenBank-	bank: GenBank 79, all bank: GenBank 79, all bank: GenBank 79, all bank: GenBank 79, all	, all , all , all	esults of the optimiz	Query sequence being compared: FLP (1-34) Number of sequences optimized: 3751	MUSMFR3 BALB/c fibroblast growth fact 4158 26 26 3.84 PIGCA24TA Sus scrofa microsatellite pol 211 25 26 3.62 SMDEXB S.mutans dextran glucosidase 1800 25 25 3.62	Fig-2 gene for fibrobla 2887 26 26 3.84	above mean **** n	Init. Opt. Sequence Name Description Length Score Score Sig. Frame	The list of other best scores is:	1. Q25185 pSW6 expression vector. 7984 34 34 5.65 (2. Q44265 pSW6 for expression of LD78 s 7859 34 34 5.65 (3. Q12154 Shuttle vector pSW6. 7859 34 34 5.65 (4. ZMICRON-B B form of the yeast 2micron p 6248 34 34 5.65 (3. Q12154)	Sequence Name Description Length Score Score Sig. Frame	4 100% similar sequences to the query sequence were found:	The scores below are sorted by initial score. Significance is calculated based on initial score.	Cut-pff raised to 17. Cut-bff raised to 18. Cut-off raised to 19.
Number of residues: 9352894 Number of sequences optimized: 3751	Times: CPU Total Elapsed 00:00:56.90 00:03:35.00	Scores: Mean Median Standard Deviation 20 21 1.11	SEARCH STATISTICS	Initial scores to save 10 Alignments to save 10 Optimized scores to save 10 Display context 0	off score	Similarity matrix Unitary K-tuple 4 Mismatch penalty 1 Joining penalty 30 Gap penalty 1.00 Window size 4 Gan size negativ 0.33	PARAMETERS	STDEV-3 -2 -1 0 1 2 3 4 5 6 SCORE!7 18 19 20 21 22 23 24 25 25			0 5-	0 10-	me -	ŧ 1	0 S 100- 0 50-	INDE COLL *	ସ ପ ଠ		R 1000-

The scores below are sorted by optimized score. Significance is calculated based on optimized score.

100% similar sequences to the query sequence were found:

N-B	Q12154		1. Q25185 psw6	Sequence Name Descr
B form of the yeast 2micron p	tle vector pSW6.	for expression of LD78	expression vector.	Sequence Name Description Length Score Score Sig. Fram
q		Ġ		F
6248	7859	7859	7984	ength
34	34	34	34	Init. Score
. 34	34	34	34	Init. Opt. Length Score Score Sig. Frame
12.64	12.64	12.64	12.64	Sig
64	64	64	64	
	_	_	_	<u> </u>

Seque	Sequence Name		h Sco	re Sc	ore	sig.	Frame
		**** 11 standard deviations above mean ****	mean	* *			
5.	5. 029100	Sequence of FLP recombination 33 33	ω	33	ω ω	11.73 0	0
		**** 6 standard deviations above mean ****	mean	* * *			
٠,	RSCALPST	Rat mRNA for calpastatin 1931 22		22	27	6.32	0
		**** 5 standard deviations above mean	mean	***			
7.	HSFGL2	Human Flg-2 gene for fibrobla 2887	7	26	26	5.42	0
œ	MUSMFR3	BALB/c fibroblast growth fact 4158		26	26	5.42	0
9.	PIGCA24TA	Sus scrofa microsatellite pol 21:		25	26	5.42	0
10.	10. RABCALPA	Rabbit calpastatin mRNA, comp 3689	9	25	26	5.42	0

FLP (1-34) Q25185 pSW6 expression vector.

```
Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10; phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss.
                                                                                                                                                                                                               Q25185 standard; DNA; 7984 BP
Q25185;
                                                                                                                                                  WO9207874-A.
                                                                                                                                                                                            pSW6 expression vector.
                                                                                                                                                          Saccharomyces cerevisae.
                                                                                                                                                                                                     .8-NOV-1992 (first entry)
```

23-OCT-1991; G01860. 24-OCT-1990; GB-023149. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Dawson KM, Edwards RM, Fallon A; WPI; 92-183627/22.

New proteins comprising active protein and integrin-affinity sequence - are antithrombotics useful in treating and preventing myocardial infarction, stroke, pulmonary embolism and deep vein

Chrombos 16

The sequence given is the yeast expression vector pSW6. It is base on the 2 micron circle from Saccharomyces cerevisae. It is a shutt vector capable of replication in both S. cerevisae and Escherichia coli as it contains the origin of replication for both organisms. also contains the leu2 gene (a yeast selectable marker) and the amipicillin Disclosure; Page 67; 101pp; English. resistant locus for selection of plasmid maintenance in E. It is a shuttle It is based Η

> Initial cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSW6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSW6 this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha- factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is the alpha-factor pro-peptide. Genes to be inserted into the percession vector must therefore have the general composition: site-alpha-factor adapter-gene-BamHI site. Sequence Score This vector has enhanced ability for passage through 7984 BP; 34 76% 0 Optimized Score 2348 A; 1698 C; 34 26 1636 G; Significance = 2303 E.coli ; 12.64 8 0 HindIII

Conservative Substitutions

Residue

Identity =

Matches

Mismatches

FLP (1-34) Q44265 pSW6 for expression of LD78 synthetic gene.

23-NOV-1993 (first entry)
pSW6 for expression of LD78 synthetic gene.
SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha;
macrophage inflammatory protein; multimer; tumour therapy;
psoriasis; hyperproliferation; yeast expression vector; Location/Qualifiers misc_difference 1773 Q44265 standard; DNA; 7859 Q44265; /*tag= a /note= "base illegible circular; ds. Saccharomyces cerevisiae. in the specification" 먥

08-UUL-1993. 08-UUL-1993. G02390. 23-DEC-1991; GB-027319. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. (BRBI-) CZADLEWSKI LG, EdWARDS RM, WO9313206-A. Gilbert RJ;

Hunter MG; WPI; 93-227322/28.

Protein with stem cell inhibition activity, e.g. LD78 or MIP-1 alpha - unable to form stable multimer higher than dodecamer,

providing better tissue penetration Disclosure; Page 159-168; 294pp; English.

An expression vector was designed to enable secretion of LD78 to the extracellular medium after expression in S. cerevisiae. Secretion aids purification and rapid analysis of LD78. The secretion signals from the yeast mating type factor alpha were used to direct export of the LD78 protein. The yeast expression vector pSW6 (NCIMB 40326) is based on the 2 micron circle from

```
Gaps
                                                      Residue Identity
                                                             Initial Score
                                                                             ည္သီလိုလိ
      GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC
                      GAAGTTCCTATTCNNNNNNNNGTATAGGAACTTC
                                                                                       S. cerevisiae.
Sequence 7859
                                                                                     Sequence
                                                                             Others;
3140
                                                u u
                                                             H
                                                                                       BP;
                                               Conservative Substitutions
                                                      Optimized Score Matches
                                                                                       2317
3160
                               30
                                                                                      ?
                                                                                       1667
                                                        8 8
                                                                                       Ç
                                                       34
26
                                                                                       1585 G;
                                                       Mismatches
                                                            Significance =
                                                                                       2289
                                                 B II
                                               12.64
8
0
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FLP (1-34) Q12154 pisclosure; Page 71; 115pp; English.

The vector is based on the 2u circle from S. cerevisiae. It is deposited in S. cerevisiae strain BJ2168 as NCIMB 40326. It is a shuttle vector capable of replication in both E. coli and S. cerevisiae and contains origins of replication for both, the leu2 gene (selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli colE1-based replicon pAT153. The vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of this fusion is under control of a galactodse regulated promoter which contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1 in E. coli K12 HW87. The plasmid can be used to construct expression vectors in which the hirudin gene is linked to a second gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide link contains a cleavage site for e.g. factor X or thrombin which can be cleaved, releasing the individual proteins which have antithrombotic activity. The enzymes which cleave the fusion protein are present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF gene can be excised by digestion with HindIII and BamHI. The plasmid was used for the expression of a synthetic hirudin HV-1 gene in E. coll KI2 HW87. The plasmid can be used to construct ex-07-DEC-1990; G01911. 07-DEC-1989; GB-027722. 07-DEC-1990; WO-G01911. (BRBI-) BRIT BIO-TECHN LTD. Q12154 standard; DNA; 7859 BP Q12154; Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; plasmid; circ occurring. See also Q12153-Q12156, Fusion protein cleavage by blood clotting enzyme – for prodn. fractions having greater antithrombotic activity for therapy a Synthetic Shuttle vector psw6 Dawson KM, Hunter MG, Czapleswski LG; Shuttle vector pSW6. (first entry) Q12158-Q12162 and Q12490 circular; ss.

Initial Score

II

ω **2**

Optimized Score

tl

3

Significance = 12.64

Sequence orgrpl

/note="2 micron replicon" 6248 BP; 1961 A; 1188 C; 1248 G;

1851 T; 0 other;

repeat_unit repeat_unit

3714..4112

/note="inverted repeat"
700..1050 /note="inverted repeat" 5570..6319

note="FLP" 'note="REP2"

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Residue Identity = Gaps =
Initial Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLP (1-34)
2MICRON-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTTCCTATTCNNNNNNNGTATAGGAACTTC
                                                                                                                                     pept
                                                                                                                                                                                             are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FLP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the A form in Genbank. Not available commercially. No antibiotic
                                                                                                                                                                                                                                                  This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that
                                                                                                                                                                                                                                                                                                                                                                                                                B form of the yeast 2micron plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                        Broach J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2MICRON-B
                                                                                                                                                                       resistance or color markers. (SUPPLIER (NONE COMMERCIAL))
                                                                                                                                                                                                                                                                                                                                                                                         Vector; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG0001;
                                                                                                                                                                                                                                                                                                                                  yeast plasmid 2u circle"; 28: 203-204 (1982).
                                                                                                      /note="REP1"
4308..5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 6248 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         form of the yeast 2micron plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
76%
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B₽;
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative Substitutions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1656 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Significance =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ę;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.64
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Residue Identity = Gaps =

76**%** 0

. FLP (1-34) Q29100

Q29100 standard; DNA; Q29100;

25-FEB-1992

misc feature

Synthetic.

й09215694-A.

label= spacer

```
FIP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development transgenes for therapeutic purposes and analysis of development claim 33; page 40; 49pp; English.

FIP recombinates is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy number of the 2-mu plasmid of S. cerevisiae during DNA replication. The inventors claim a mammalian recombination system in which the FIP recombinase is pref. 029101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair spacer (see 029100). The nucleotides in the spacer region can be replaced with any other combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of
GAAGTTCCTATTCNNNNNNNNGTATAGGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1992. U01899. 06-MAR-1992; U01899. 08-MAR-1991; US-666252. (SALK ) SALK INST BIOLOGICAL STUDIES. (SALK ) SALK INST GM; WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of FLP recombination target site FLP recombinase; site-specific integration system; gene gene inactivation; as.
                                                                                                                                                                                apparently missing base would be C. Sequence 33 BP; 11 A; 5 C;
                                                                                                                                                                                                                          the FRT has only 12 base pairs on the 3' end of the spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of FLP recombination target site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 14..21
                                                                                            Optimized Score = 33
Matches = 25
Conservative Substitutions
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                                                                                                                     Mismatches
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                                                                                                                                      Significance
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                                                                                                 11.73
8
0
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                                                                                                                     Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD
REFERENCE
AUTHORS
                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSCALPST
               Sgo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full automatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishida,S., Emori,Y. and Suzuki,K.
Rat calpastatin has diverged primary sequence from other mammalian calpastatins but retains functionally important sequences
Biochim. Biophys. Acta 1088, 436-438 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-NOV-1990) Y. Emori, BIOCHEMISTRY, FACULTY OF SCIENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat mRNA for calpastatin X56729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fheria; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1931)
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                                                                                                                                                                                                                               671
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                                                                                                                     65%
22
                                                                                                                                                                                                                                                KGKKTSSSKASKNEEKTKDSSKKTEEVPKPKVDEDAT*
                                                                                                                                                                                                                                                                       PPPGTERRDKELDDALDELSDSLGQRQPDPDENKPLDDKVKEKIKAEHSEKLGERDDT
IPPEYRHLLDNDGKDKPEKPLDKEHREAGQDQDPIDALSEDLDSCPPTTETSQNTTKE
                                                                                                                                                                                                                                                                                                              KPLLPEPEETSKCLSESELIGELSADFVQPTYQEKPSMPAAKIKKGVVPDDAVETLAR
SLGTRKEDPEDEKSLVDKVKEKAKEEDHEKLGEKEETIPPDYRLEIVKDKDGKPLLPK
EAEEQLPPLSDDFLLDALSQDFSSPANILSLGFEDAKLSAAVSETVSQVPAPSNHTAA
                                                                                                                                                                                                                                                                                                                                                                            QALSDSLGTRQPDPQSHLRQAKQVKEAKAKEERQEKCGEDEDTVPAEYRLKPAKDKDG
                                                                                                                                                                                                                                                                                                                                                                                                  VATASDEVVYKKKEKKSLTPTLPMESTLNKLSDKSGVNAALDDLIDTLGECEDTNKDD
PPYTGPVVLDPMDSTYLEALGIKEGTIPPEYRKLLEKNEAITGPLPDSPKPMGIDHAI
DALSSDFTCSSPTGKQTEKEKSTGESSKAQSAGVTRSAVPPQEKKRKVEEEVMNDQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus sp."
/tissue_type="liver"
/clone_lib="cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \primetrans\overline{1}ation="MSTTGAKPPVIHEKKPKGKPKEGSETKFQDAPSADGESVAGDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="calpastatin/CANP inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="calpastatin/CANP inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOKYO 113, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
cheria; Rodentia; Myomorpha; Muridae; Murinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 1931)
                                                                                                                                                                                                                             406 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANP inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1931 þp
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Matches
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                                                                                                                       Substitutions
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                                                                                                                                         Significance = Mismatches =
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                                                                                                                         11 11
                                                                                                                       6.32
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0
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A PROPERTY OF THE PROPERTY OF

6. FLP (1-34)

FLP (1-34) HSFGL2

Human Flg-2 gene for fibroblast growth factor rece

GAAGGGACTATTC-CTCCAGAGTATAGGAAACTTC X 400 410 420 X

GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT
X 10 20 30 X

Residue Identity

H H H

33 75**%** 0

Initial

ORIGIN ORIGIN Initial Score = 26 Optimized Score = 26 Significance = 5.42 Residue Identity = 58% Matches = 20 Mismatches = 14 Gaps = 0 Conservative Substitutions = 0	MKIADFGLARDVINLDYKKTINGELPVKWIAEGHALPUKVITHODIVWSFGVLIWELF TLGGSPYPGIPVEELFKLIKEGHADDKPASCTEDLYMIHEGUNIAVPSORPTFGOLVE DLDRILTVTSTDEYLDLSVPFEQYSPGGODTPSSSSSGDDSVFTHDLLPPGPPSNGGP RT* BASE COUNT 592 a 834 c 891 g 570 t	GYYSCOBILITRATICHE SVRVTDADS SGDDEDGEDVAEDTGAPY WIRPERADKKLLAV GYASCOBILITRATICHE SVRVTDADS SGDDEDGEDVAEDTGAPY WIRPERADKKLLAV PAANTVEERCEPAAGNEPES I SWILKNGKEE FROGHELIGGIKLRHOOWSLIVÆS SVRVESDRG NYTCVVENKEGS I RQTYTLDVLERSPHRP I LOAGLPANOTA I LGSDVEFHCKVYSDAO PHI QWILKHVEVNGSKVGEPDGTPYDTVLKTBAGNATTDKELEVLSLHNVTEDAGSYTGL AGNS I GF SHHSAWLVVLPAEEELMETDEAGSVYAGVLSYGVVFF I FI LVVAAVI I LCRL RSPPKRCILGSPTVHKVSEFP I KRQVSLESNSSMSNTP LVRLAELSGGEOVLANVSE LELPADPKWELSKTELT I CKEP LGEGGFGQVVMAEA I GIDKDRTAKEVITVAVKMLKDDA TDKD LSDLVSEKEMRKMI GKHKNI I NLLGACTGGGPLYVLVEYAAKGNLEEF LEARRP PGMDYSFDACRLPEEQLITCKD LVSGAYQVARGMEY LASQKG I HEDLAARNVLVTEDNV		,	N) >	ENTAL	mHNA 1288/ /gene≕"Flg-2"		Source 1288/ /organism="Homo sapiens" /tissue type="skin"	Oncogene full auto	2 (bases 1 Avivi,A., Zi Flg-2, a nev receptor	Submitted 76100 Reho		SOURCE numan ORGANISM Homo sapiens Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.	TION ION DS
Initial Score = 26 Optimized Score = 26 Significance = 5.42 Residue Identity = 58% Matches = 20 Mismatches = 14 Gaps = 0 Conservative Substitutions = 0 X 10 20 30 X	158 anism="Mus musculus" 107 c 1205 g 935 t	PHIOWIKHVEVNOSKVOPDGTFYVTVLKTAGANTTDKELEVLSIHNVTFEDAGEYYCL AGNSIGFSHHSAMIVVLPAEEELMETDEAGSVYAGVLSYGVVFFLFILVVAAVILCRL RSPPKKGLGSPTVHKVSRFPLKROVSLESNSMSNIFPLVRIARLSSGEGEVLANVSE LELPADPKWELSRTRLTIGKPLGEGGFGQVVMAEAIGIDKDRTAKPVTVAVKMLKDDA TDKDLSDLVSEKEMMKMIGKHRWI INLLGACTQGGFLYVLVEYAAKGNLREFLARRP PGMDYSFDACRLPEEQLTCKDLVSCAYQVARGMEYLASGKCIHBDLARMVLVTEDNV MKILDFGLARDVHNLDYYKKTTNGRLPVXWMAAPEALFDRVYTHOSDVWSFGVLLWEIF TPGGPSPYPGIPVEELFKLLKEGHRMDKPASCTHDLYMIMRECWHAVPSQRPTFKQLV EDLDRI"	/translation="MVVPACVLVFCVAVVAGATSEPPECEGRVVRRAAEVECYEPSOQ EQVAFGSGDTVELSCHPPGGAPTGPTVMAXDGTGLVASHILIVGPQALQVLNASHEDA GVYSCQHRLTRRVLCHFSVRVTDAPSGDDEDGEDVAADTGAPYMTRPERMDKKLAN GVYSCQHRLTRRVLCHFSURVLDAFSGDENGETHGGIKLRHQQWSLIVMESVVPSDRG PAANTVRERCPAAGNPTPSISWLKNGKEFRGEHRIGGIKLRHQCWSLIVMESVVPSDRG NYTCVVENKFGSIRQTYTLDVLERSPHRPILQAGLPANQTAILGSDVEFHCKVYSDAQ	<pre>/gene= mrss /product="fibroblast growth factor receptor 3" /codon_start=1</pre>	CDS 2272632 CDS 2272632	\$19_peptide		Jactor receptors 1 and 3 JOURNAL J. Biol. Chem. 267, 16305-16311 (1992)		OKOANISM MUS MUSCULUS EUKaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. REFERENCE 1 (bases 1 to 4158)		m m	LOCUS MUSMFR3 4158 bp ss-mRNA ROD 03-SEP-1992 DEFINITION BALB/c fibroblast growth factor receptor 3 (mFR3) mRNA, complete	8. FLP (1-34) MUSMFR3 BALB/c fibroblast growth factor receptor 3 (mFR3)	X 10 20 30 X GAAGTTCCTATTCNNNNNNNGTATAGGAACTTC

10. FLP (1-34) RABCALPA DEFINITION ACCESSION REFERENCE FEATURES KEYWORDS TITLE ORGANI SM STANDARD AUTHORS JOURNAL calcium-dependent cysteine protease; calpastatin. Rabbit lung or heart, cDNA to mRNA, clones lambda-C1-[2,311,11,21,213,413,408]. Oryctolagus cuniculus Chordata; Vertebrata; Mammalia; Theria; Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Rabbit calpastatin mRNA, complete cds. M16476Emori,Y., Kawasaki,H., Imajoh,S., Imahori,K. and Suzuki,K. Endogenous inhibitor for calcium-dependent cysteine protease contains four internal repeats that could be responsible for its multiple reactive sites Eutheria; Lagomorpha; Leporidae. 1 (bases 1 to 3689) RABCALPA full automatic Rabbit calpastatin mRNA, complete cds. Natl. Acad. Sci. U.S.A. 84, Location/Qualifiers 3689 bp ss-mRNA 3590-3594 (1987) MAM 15-JUN-1989

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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results file Lipi.res made by low on Tue 1 Feb 94 15:27:19-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                     1000-
                                                                                                                                                                                                           5000-
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ta bank: EMBL-NEW 11, all MANMALIAN entries
ta bank: EMBL-NEW 11, all OTHER MAMMALIAN
ta bank: EMBL-NEW 11, all PRIMATE entries
ta bank: EMBL-NEW 11, all PRIMATE entries
ta bank: EMBL-NEW 11, all RODENT entries
ta bank: EMBL-NEW 11, all RODENT entries
ta bank: GenBank 79, all OTHER MAMMALIAN entries
ta bank: GenBank 79, all OTHER MAMMALIAN entries
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PRIMATE entries
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all OTHER MAMMALIAN entries
all OTHER_VERTEBRATE entries
                                                                                                                                                                                                                                                                                                                                                                          Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                     Number of residues:
Number of sequences searched:
Number of scores above cutoff:
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                                                                                                                                                                                                                                                         Scores:
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f raised to 8. raised to 10. f raised to 13. f raised to 14. f raised to 15. f raised to 15. f raised to 16. f raised to 17.
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112413
3802
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Joining penalty
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4
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Results of Data bank : EM Data bank : EM	Query sequence being compared: Number of sequences optimized:	9. SMDEXB 10. RATQLIKEB		6. DOGRABSA	2. NS3100	4. 025185	3. Q12154	2. 044265	Sequence Name		The list of other best scores is:	1. 2MICRON-B	Sequence Name	A 100% similar se	The scores below Significance is c	Cut off raised to 18.
Results of the optimized comparison of FLP' (1-34) with: Data bank: EMBL-NEW 11, all MAMMALIAN entries Data bank: EMBL-NEW 11, all OTHER_MAMMALIAN entries	FLP' (1	S.mutans dextran glucosidase Rattus norvegicus Q-like gene	Mouse house-keeping protein m	C.familiaris GTP-binding prot Human complement component C4	**** 3 standard deviations above mean ****	psw6 expression vector.	Shuttle vector psw6.	**** 4 standard deviations above mean **** pSW6 for expression of LD78 s 7859 31	Description	•	best scores is:	B form of the yeast 2micron p	Description	A 100% similar sequence to the query sequence was found:	The scores below are sorted by initial score. Significance is calculated based on initial score.	18.
LP' (1- les N entr:	1-34) 3802		. E		s above	. 7		s above	Len			6 d	Len.	was for	ore.	
-34) wi				796 848	e mean			ve mean 7859	Length Score Score	Ini		6248	Init. Opt.	ind:		
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STDEV-3 SCORE18	. 0	1 1 1	1	יט	١ (10-	•	1 1	1 2	,	50 1	S 100-	9 O Z	пОк		F 1000-
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Results of the optimized comparison of FLP' (1-34) with: Data bank: EMBL-NEW 11, all MANMALIAN entries Data bank : EMBL-NEW 11, all PRIMATE entries Data bank : EMBL-NEW 11, all PRIMATE entries Data bank : GenBank 79, all MANMALIAN entries Data bank : GenBank 79, all OTHER MANMALIAN entries Data bank : GenBank 79, all OTHER TATE Data bank : GenBank 79, all OTHER TERTEBRATE entries Data bank : GenBank 79, all PATENT entries Data bank : GenBank-NEW 11, all OTHER MANMALIAN entries Data bank : GenBank-NEW 11, all PRIMATE entries Data bank : GenBank 6.4, all entries Data bank : VectorBank 6.4, all entries Data bank : VectorBank 6.4, all entries

	Initial scores to save Optimized scores to save	oup	Similarity matrix Uni Mismatch penalty Gap penalty Gap size penalty
SEAF	10	سر سو	Unitary 1 1.00 0.33
SEARCH STATISTICS	Alignments to save Display context	Number of randomizations	K-tuple Joining penalty Window size
	0	L	30 4

PARAMETERS

266-

 Scores:
 Mean 21
 Median 22
 Standard Deviation 1.11

 Times:
 CPU 700:00:57.94
 Total Elapsed 00:03:32.00

Number of residues:
Number of sequences optimized:

9177971 3802

202202

ELLOW

The scores below Significance is c calculated are sorted by optimized score. ulated based on optimized score.

A 100% similar sequence ç the query sequence was found:

1 0

1 0

ther best s Descri **** PSW6 Shutt PSW6 Shutt PSW6 **** Seque **** O Mouse **** A C.faman A Human A Ratt C.faman B Ratt C. Batt C.	Sequence Name Description	Init. Opt. Length Score Score	Init. Opt. Score Scor	Opt. Score	Sig. Frame	ame
ist of other best s ince Name Descri **** Q44265 PSW6 Q12154 Shutt Q25185 PSW6 Q25185 PSW6 Q29100 Seque MUSHCPRO **** DOGRAB5A Human HUMC4BAA Human HUMC4BAA Human RATCGEMIACA Ratt C	N-B B form of the yeast 2micron p	6248	34	34	34 11.75 0	0
Descri **** psw6 psw6 psw6 psw6 psw6 psw6 psw6 psw6	other best scores is:					
Q44265 pSW6 Q12154 Shutt Q25185 pSW6 Q25185 pSW6 Q25187 Seque MUSHKPRO MOUSE MUSHKPRO MOUSE ANTOTIKEN BATCOMMARA RATCOMMARA RATCOMMA	Description	Init. Opt. Length Score Score	ore :	Init. Opt. Score Score	Sig. Frame	ame
Q44265 pSW6 Q25185 pSW6 Q25185 pSW6 Q25180 ***** Q29100 ***** Q29100 ***** MOUSHKPRO MOUSE MUSHKPRO MOUSE MUSHKPRO C.fam HUMC4BAA Human HUMC4BAA Human RATCGMIAC3 Rat c	**** 9 standard deviations above mean ****	bove mean	*	*		
Q12154 S Q25185 p Q25185 p Q29100 S MUSHKPRO M DOGRAB5A C HUMC4BAA H RATCIMIACB R RATCIMIACB R	pSW6 for expression of LD78 s	7859	31	31	9.04	0
Q25185 P Q29100 S MUSHKPRO M DOGRAB5A C HUMC4BAA H RATCIMIACB R BATCIMIAC B BATCI I KEB	Shuttle vector pSW6.	7859	31	31	9.04	0
Q29100 S MUSHKPRO M DOGRABSA G HUMC4BAA H RATCIMIAC B BATCITET B B	psw6 expression vector.	7984	31		9.04	0
Q29100 seque #### MUSHKPRO Mouse #### DOGRAB5A C.fam HUMC4BAA Human RATCGM1AC3 Rat C	**** 8 standard deviations above mean	bove mean	*			•
MUSHKPRO Mouse **** DOGRAB5A C.fam HUMC4BAA Human RATCGM1AC3 Rat c	<pre>Sequence of FLP recombination 33 **** 5 standard deviations above mean</pre>		30	* 30	8.14	0
DOGRAB5A C HUMC4BAA H RATCGM1AC3 R	Mouse		26	27	5.42	0
DOGRAB5A HUMC4BAA RATCGM1AC3		bove mean	*			•
HUMC4BAA RATCGM1AC3	5A C.familiaris GTP-binding prot	796	26	26	4.52	0
RATCGM1AC3		848	26	26	4.52	0
BATOI IKEB		828.	18	26	4.52	0
WIGHTNESS		2043	25	26	4.52	0

FLP' (1-34) 2MICRON-B B form of the yeast 2micron plasmid.

2MICRON-B standard; DNA; 6248 BP

IG0001;

09-SEP-1986

B form of the yeast 2micron plasmid

Vector; circular.

Broach J.R.;
"The yeast plasmid 2u circle";
Cell 28: 203-204 (1982).

This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FLP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the form in Genbank. Not available commercially. No antibiotic

> Residue Identity = Gaps = 30 X
> GAAGTTCCTATACNNNNNNNGAATAGGAACTTC GAAGTTCCTATACTTTCTAGAGAATAGGAACTTC pept pept pept /note="2 micron replicon" Sequence 6248 BP; 1961 A; 1188 C; 1248 G; Key repeat_unit repeat_unit resistance or color markers. (SUPPLIER (NONE COMMERCIAL)) Score /note="REP1" 4308..5197 /note="REP2" 5570..6319 /note="inverted repeat"
> 3714..4112 341..938 /note="inverted repeat"
> 700..1050 3769..2644 Location/Qualifiers 'note="FLP" Optimized Score Matches Conservative Substitutions 11 11 1851 34 26 Mismatches T; 0 other; Significance 11 11.75 8 0

FLP' (1-34) Q44265

Q44265 standard; DNA; 7859 BP. Q44265; 23-NOV-1993 (first entry) pSW6 for expression of LD78 synthetic gene.

psoriasis; hy circular; ds. pSW6 for expression of LD78 synthetic gene.
SCI; stem cell inhibition; LD78, kCT2; MIP-lalpha;
BCI; stem cell inhibition; LD78, multimer; tunour therapy;
macrophage inflammatory protein; multimer; tunour therapy;
psoriasis; hyperproliferation; yeast expression vector;

misc_difference 1773 Saccharomyces cerevisiae. ocation/Qualifiers

/note= "base illegible in the specification" WO9313206-A. /*tag=

23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Craig S, Czaplewski LG, Edwards R Hunter MG; WPI; 93-227322/28. Edwards RM,

Gilbert RJ;

Protein with stem cell inhibition activity, e.g. LD78 or MIP-1 alpha - unable to form stable multimer higher than dodecamer,

providing better tissue penetration Disclosure; Page 159-168; 294pp; English.

An expression vector was designed to enable secretion of LD78 to the extracellular medium after expression in S. cerevisiae.

Secretion aids purification and rapid analysis of LD78.

SIOD

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Residue
                                                                                       Initial Score
                                                                                                             ৪৪৪৪৯৯
          GAAGTTCCTATACNNNNNNNGAATAGGAACTTC
GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC
X 3140 3150 3160 X
                                                                                                                                        The secretion signals from the yeast mating used to direct export of the LD78 protein. vector pSW6 (NCIMB 40326) is based on the 2
                                                                                                                       Sequence
                                                                                                                                S. cerevisiae
                                                                          Identity
                                                                                                             Others;
                                                                    0 0 0
                                                                                                                       7859 BP;
                                                                31
70%
0
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                                                                                                                       2317 A;
                                                                                                                       1667 C;
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                                                                                                                                             The yeast expression micron circle from
                                                                                                                                                      type factor alpha were The yeast expression
                                                                             24
                                                                                                                       1585 G;
                                                                  Significance = Mismatches = =
                                                                             Mismatches
                                                                                                                        2289 T;
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CC shuttle vector capable of replication in both E. coli and S. cerecce (selectable marker), and an ampicillin resistant locus. The E. coli (selectable marker), and an ampicillin resistant locus. The E. coli (sequences are derived from E. coli (colE1-based replicon pAT153. The CC vector contains an alpha factor pre-pro-peptide gene fused in frame CC to the gene for epidermal growth factor (EGF). The expression of CC this fusion is under control of a galactodse regulated promoter and the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF CC gene can be excised by digestion with HindIII and BamHI. The plas-CC mid was used for the expression of a synthetic hirudin HV-1 gene CC in E. coli K12 HW87. The plasmid can be used to construct expression vectors in which the hirudin gene is linked to a second CC gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide CC link contains a cleavage site for e.g. factor X or thrombin which CC can be cleaved, releasing the individual proteins which have anti-cc thrombotic activity. The enzymes which cleave the fusion protein cc are present at the site of the target thrombus so the active agents . FLP' (1-34) Q12154 Disclosure; Page 71; 115pp; English.
The vector is based on the 2u circle from S. cerevisiae.
deposited in S. cerevisiae strain BJ2168 as NCIMB 40326. 07-DEC-1990; G01911. 07-DEC-1989; GB-027722. 07-DEC-1990; WO-G01911. (BRBI-) BRIT BIO-TECHN LTD. Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and Dawson KM, Hunter MG, Czapleswski LG; WPI; 91-208151/28. Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; plasmid; circular; Q12154 standard; DNA; 7859 BP Q12154; prophylaxis. Shuttle vector pSW6 27-JUN-1991. №09109125-A. 7-SEP-1991 (first entry) Shuttle vector pSW6 cerevisiae. It is a

Initial Score

n

31

Optimized Score =

31

Significance =

9.04

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9.04
10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4. FLP' (1-34)
Q25185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial
    នននិន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC X 3140 3150 3160 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGTTCCTATACNNNNNNNNGAATAGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also
Sequence
the alpha-factor pro-peptide. Genes to be inserted into the pSW6 expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BamHI site.

Sequence 7984 BP; 2348 A; 1698 C; 1635 G; 2303 T;
                                                                                                                                                                                                coli as it contains the origin of replication for both organisms. It also contains the leu2 gene (a yeast selectable marker) and the amipicullin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced ability for passage through E.coli and this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha-factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under
                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins comprising active protein and integrin-affinity sequence - are antithrombotics useful in treating and preven myocardial infarction, stroke, pulmonary embolism and deep v
                                                                             cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSM6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of
                                                                                                                                           the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is
                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 67; 101pp; English.
The sequence given is the yeast expression vector pSW6. It is based on the 2 micron circle from Saccharomyces cerevisae. It is a shuttle vector capable of replication in both S. cerevisae and Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1991; G01860.
24-OCT-1990; GB-023149.
(BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q25185 standard; DNA; 7984 BP. Q25185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are released specifically at the place where clot formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dawson KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pSW6 expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09207874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisae
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183627/22.
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7859 BP; 2317 A; 1656 C; 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing deep vein
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Resigue Gaps

Identity

FLP' (1-34) Q29100

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FIP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development S Claim 33; Page 40; 49p; English.

FIP recombinates is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy number of the 2-mu plasmid of S. cerevisiae during DNA replication. The inventors claim a mammalian recombination system in which the FIP recombinase is pref. 029101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair spacer (see 029100). The nucleotides in the spacer region can be replaced with any other combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of the FRT has only 12 base pairs on the 3 end of the spacer. The apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; 6 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGTTCCTATACNNNNNNNGAATAGGAACTTC
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X 3140 3150 3160 V
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06-MAR-1992; U01899.
06-MAR-1991; US-666252.
(SALK ) SALK INST BIOLOGICAL STUDIES.
090rman SV, Wahl GM;
WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               029100 standard; DNA; 33 BP. 029100; 25-FEB-1992 (first entry) Sequence of FLP recombination target site FLP recombinase; site-specific integration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of FLP recombination target site
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                        Conservative Substitutions
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JOURNAL
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mRNA, clone II.
Canis familiaris
                                           C.familiaris
                                                                                              M35520
                                                                                                           C. familiaris GTP-binding protein (rab5) mRNA, complete cds.
                                                                   GTP-binding protein.
                                                                                                                                   DOGRAB5A
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                                                                                                                                                                          .familiaris GTP-binding protein (rab5) mRNA,
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GRVELMEVSEKEFRKLIAFPKRPDLYQVMAVLUQVACOVKFLHMEDWSSFSVHENG
HLEKSKHGESVNLIKQNLYLVBHTFRETLFTENLSPLNYDIFFHLVKHCFGKRNAPII
RHLRSLSTVDPINILRQIRKNPGDTAARMYPHDFKKLFETIEQSEDSVFKWIYDVCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon start=1
/translation="MRGPAMRLPPRLALSALARGPSCILGSGAATRKDWQTRNGRGFS
/translation="MRGPAMRLPPRLALSALARGPSCILGSGAATRKDWQTRNGRGFS
DFNLEPLPDSDLEESSPWTSRNRSEPTRHIACKKAAANLVRDLEEHONPSRQILLECN
DFNLEPLPDSDLEESSFWTSRNRSEPTRHIACKKAAANLVRDLEEHONPSRQIE
PGPGILTGALLKAGARVVAFESEKTFIPHLEPLORGRANMDGELQVVHCDFFKMDPRYQEV
PGPGILTGALLKAGARVVAFESEKTFIPHLEPLORGRANMDGELQVVHCDFFKMDPRYQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
478 c 535 g 671
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                                                (strain Madin-Darby; Cocker spaniel) kidney, cDNA
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                                                                                                                                     796 bp ss-mRNA
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21
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misc_feature

/label= spacer WO9215694-A.

Synthetic.

6. FLP' (1-34)

Residue Initial

Identity

GAAGTTCCTATACNNNNNNNNGAATAGGAACTT

GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT X 10 20 30 X

REFERENCE AUTHORS TITLE

Chavrier, P., Parton, R.G., Hauri, H.P., Sim localization of low molecular weight GTP exocytic and endocytic compartments Cell 62, 317-329 (1990)

Simons, K. and Zerial, TP binding proteins t

0, M

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Carnivora; Caniformia; Canoidea; Canidae.

Caniformia;

Eutheria; Carnivora;

ORGANISM

JOURNAL STANDARD

full automatic

/codon start=1 /codon start=1 /note="C4b-binding protein beta-chain signal peptide" mat_peptide 80784 /gene="C4BPB"	FEATURES Location/Qualifiers <pre></pre>	Chain JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 1183-1187 (1990) STANDARD full automatic COMMENT Draft entry and printed sequence for [1] kindly submitted by A.Hillarp, 18-NOV-1989.		IOCUS HUMC4BAA 848 bp ss-mRNA PRI 15-JUN-1990 DEFINITION Human complement component C4b-binding protein beta-chain (C4BP) RRNA, complete cds. ACCESSION M29964 KEYWORDS complement component C4b-binding protein. SOURCE Human liver, CDNA to mRNA, clones C1 and A8.	8. FLP' (1-34) HUMC4BAA Human complement component C4b-binding protein bet	X 10 20 30 X GAAGTTCCTATACNNNNNNGAATAGGAACTTC	Initial Score = 26 Optimized Score = 26 Significance = 4.52 Residue Identity = 58% Matches = 20 Mismatches = 14 Gaps = 0 Conservative Substitutions = 0	/translation="MANRGATRENGENIGNKICQFKLVLLGESAVGKSSLVLRPVKGQ FHEFQESTIGAAFLTQTVCLDDTTVKFELWDTAQGERYHSLAFWYYGDG TNEESFARKNWYKELDROASPNIVLALSGNKADLANKRAVDPÖLGAGYADDNSLLFM ETSAKTSMNVNEIFMAIAKKLPKNEPQNPGANSARGRGVDLTEFTQPTRSQCCSN" 80urce 1796 //organism="Canis familiaris" BASE COUNT 267 a 163 c 174 g 192 t ORIGIN	Base-pairs 664 to 711 form a synthetic peptide used to raise antibodies. FEATURES Location/Qualifiers CDS 101.768 /note-="GTP-binding protein; (rab5)" /codon start=1	COMMENT Draft entry and computer-readable sequence for [Cell (1990) In press] kindly submitted by P.Chavrier, 22-JUN-1990.
re = (Intron <1>828 intron <1>828 source 1828 source /organism="Rattus norvegicus" BASE COUNT 193 a 255 c 190 g 190 t	L J. Biol. RD full auto Praft ent by W.Zimm	ORGANISM Rattus norvegicus Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. REFERENCE 1 (basse 1 to 828) AUTHORS Rebstock, S., Lucas, K., Thompson, J.A. and Zimmermann, W.A. TITLE cDNA and gene analysis imply a novel structure for a rat	LOCUS RATCGMIAC3 828 bp ds-DNA DEFINITION Rat carcinoembryonic antigen-related protein (CGMI) gene, intron B. ACCESSION M32478 JO5417 KEYWORDS carcinoembryonic antigen-related protein. SEGMENT 3 of 8 SOURCE R.norvegicus (strain Sprague-Dawley) liver DNA, clone lambda-rncGM1-1.	9. FLP' (1-34) RATCGM1AC3 Rat carcinoembryonic antigen-related protein (CGM1	X 10 20 30 X GAAGTTCCTATACNNNNNNIGAATAGGAACTTC	Initial Score = 26 Optimized Score = 26 Significance = 4.52 Residue Identity = 58% Matches = 20 Mismatches = 14 Gaps = 0 Conservative Substitutions = 0	GTYYCIKGYHLVGKKTLFCNASKEWDNITTECRLGHCPDPVLVNGEFSSSGPVNVSDK ITFMCNDHYILKGSNRSQCLEDHTWAPPFPICKSRDCDPPGNPVHGYFEGNNFTLGST ISYYCEDRYYLVGVGDQCVDGEWSSALFVGKLIQEAFKPECEKALLAFQESKNLCEA MENFMQQLKESGMTMEELKYSLELKAELKAKEL* source 1.848 /organism="Homo sapiens" BASE COUNT 229 a 174 c 226 g 219 t ORIGIN	/note="gca in clone C1; no codon at 86 in clone A8" 29787 29787 /gene="C4BPB" /note="C4b-binding protein beta-chain precursor" /codon_start=1 /translation="MFFWCACCIMVAWRVSASDAEHCPELPPVDNSIFVAKEVEGQIL	<pre>/codon start=1 /note="C4b-binding protein beta-chain" variation 8688 /gene="C4BPB"</pre>

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10. FLP' (1-34)
RATQLIKEB
                                                                                                           Initial Score = Residue Identity =
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STANDARD
COMMENT
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polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus male adult liver DNA.
Rattus norvegicus
Eutkaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (bases 1 to 2043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATQLIKEB 2043 bp ds-DNA
Rattus norvegicus Q-like gene sequence.
L16013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic structure and organization of a Q-like gene in the grc-G/C region of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rushton, J.J., Misra, D.N., Kunz, H.W., Cortese Hassett, A.L. and Gill, T.J.III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full automatic *Locus = RT(2.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus Q-like gene séquence.
                                                                                                                                                                          387
                                                                                                                                                                                                                                                                                                                          Iocation/Qualifiers
86.91
/note="this polyadenylation signal was selected because of its similarity to RT1.0; putative"
1013.1264
/note="this 252 nucleotide repeat alters the DNA conformation and is associated with at least one rat MHC class I sequence; putative"
                                                                                                                                                                     /haplotype="r21"
/tissue_type="liver"
/sequenced_mol="DNA"
a 558 c 449 g
                                                                                              25 Optimized Score 58% Matches 0 Conservative Sub
                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                               note="ATGC repeat noted but absent in the RT1.0 gene;
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		411	of the optimized comparison of FLP1 (1-34) of the optimized comparison of FLP1 (1-34) EMBL-NEW 11, all OTHER MAMMALIAN entries EMBL-NEW 11, all PRIMATE entries EMBL-NEW 11, all PRIMATE entries GenBank 79, all MAMMALIAN entries GenBank 79, all OTHER MAMMALIAN entries GenBank 79, all OTHER VERTEBRATE entries GenBank 79, all PRIMATE entries GenBank-NEW 11, all OTHER VERTEBRATE entries GenBank-NEW 11, all OTHER TOTHER MAMMALIAN entries GenBank-NEW 11, all PRIMATE entries GenBank-NEW 11, all entries GenBank-NEW 13, all entries UEMBL 36 79, all entries						RABCALPA Rabbit calpastatin mRNA, comp Q23917 Taf DNA polymerase I coding s DOGRAB5A C.familiaris GTP-binding prot N82201 Beta-amylase from plant seed. sequence being compared: FLP1' (1-34) of sequences optimized:	keeping protein i statin mRNA, com merase I coding GTP-binding pro	**** 4 standard deviations pSW6 for expression of LD78 s Shuttle vector pSW6. pSW6 expression vector. Sequence of FLP recombination **** 3 standard deviations	Description	r best scores is:	B form of the yeast 2micron p	Description	sequence to the query sequence was		to 17.
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The accres below are sorted by optimized score. Significance is calculated based on optimized s score

100% similar sequence to the query sequence was found:

10. Q23917	•	8. RSCALPST	OCCASB5		6. MUSHKPRO		5. Q29100				2. Q44265		Sequence Name	The list of othe	1. 2MICRON-B	Sequence Name
Taf DNA polymerase I coding s	Human histone H2A.Z gene, ups 3088 17	Rat mRNA for calpastatin	Rabbit DNA for 5'flanking reg	**** 5 standard deviations above mean ****	Mouse house-keeping protein m 2415	**** 6 standard deviations above mean ****	Sequence of FLP recombination	**** 7 standard deviations above mean ****	pSW6 expression vector.	Shuttle vector pSW6.	psw6 for expression of LD78 s	**** 8 standard deviations above mean ****	Description	The list of other best scores is:	B form of the yeast 2micron p 6248	Description
4286	3088 bove me:	1931	2157	bove mea	2415	bove mea	33	bove mea	7984	7859	7859	bove mea	Init. Opt. Length Score Score		6248	Init. Opt. Length Score Score Sig. Frame
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4.21	5.05	5.05	5.89		6.73		7.58		8.42	8.42	8.42		Sig. Frame		13.47	Sig. Fr
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FLP1' (1-34)

2MICRON-B Ħ form of the yeast 2micron

IG0001; 2MICRON-B standard; DNA; 6248 BP

09-SEP-1986

B form of the yeast 2micron plasmid

Vector; circular.

Broach J.R.;
"The yeast plasmid 2u circle";
Cell 28: 203-204 (1982).

This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FIP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the A form in Genbank. Not available commercially. No antibiotic

> Residue Identity Initial 3860 Sequence 6248 orgrpl pept pept Key repeat_unit repeat_unit resistance or color markers. SUPPLIER (NONE COMMERCIAL)) Score 3870 /note="REP2" 5570..6319 4308..5197 H H 34 100% 0 /note="2 micron replicon" BP; 1961 A; 1188 C; 1248 G; /note="inverted 3714..4112 /note="inverted repeat" 700..1050 3769..2644 Location/Qualifiers 'note="REP1" note="FLP" Matches = 34 Conservative Substitutions Optimized Score 3890 G; 1851 34 34 Significance Mismatches Τ, 0 other; 13. .47

FLP1' Q44265 (1-34)pSW6 for expression of LD78 synthetic gene

Q44265 standard; DNA; 7859 Q44265; BP.

23-NOV-1993 (first entry)

pSW6 for expression of LD78 synthetic gene. SCI; stem cell inhibition; LD78; ACTZ; MIP-lalpha; macrophage inflammatory protein; multimer; tumour therapy;

circular; ds. psoriasis; hyperproliferation; yeast expression vector; Saccharomyces cerevisiae

WO9313206-A.

/*tag= a /note= "base illegible in the specification*

misc_difference 1773

Location/Qualifiers

08-JUL-1993.
08-JUL-1993.
23-DEC-1992; G02390.
23-DEC-1991; GB-027319.
23-DEC-1992; GB-021587.
14-CCT-1992; GB-021587.
(BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Craig 5, Czaplewski LG, Edwards RM,

Gilbert

2

WPI; 93-227322/28.

Hunter MG;

Protein with stem cell inhibition activity, e.g. LD78 alpha - unable to form stable multimer higher than dod dodecamer, or MlP-1

providing better tissue penetration
Disclosure; Page 159-168; 294pp; English.
An expression vector was designed to enable secretion of LD78
the extracellular medium after expression in S. cerevisiae. Secretion aids purification and rapid analysis of LD78



14

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Residue
                                                                                                         888888
GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC
X 3140 3150 3160 X
                                 GAAGTTCCTATACTTTCTAGAGAATAGGAACTTC
                                                                                                                                         The secretion signals from the yeast mating type factor alpha were used to direct export of the LD78 protein. The yeast expression vector pSW6 (NCIMB 40326) is based on the 2 micron circle from
                                                                                                                            vector pSW6 (NCIMB 403
S. cerevisiae.
                                                                                                                    Sequence
                                                                        Identity
                                                                                                         Others;
                                                                                   Score
                                                                  a a a
                                                                                                                    7859 BP;
                                                                 82%
0
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                                                                                                                                        ort of the LD78 p
40326) is based
                                                                         Optimized
Matches
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                                                                                                                    2317 A;
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                                                                 Substitutions
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28
                                                                                                                    1585 G;
                                                                            Mismatches
                                                                                     Significance
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                                                                  8.42
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FLP1' Q12154 Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy a Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; plasmid; circular; ss Q12154 standard; DNA; 7859 BP Q12154; prophylaxis. Dawson KM, Hunter MG, Czapleswski LG; WPI; 91-208151/28. 07-DEC-1990; WO-G01911. 07-DEC-1989; 07-DEC-1990; G01911. 27-JUN-1991. WO9109125-A. Synthetic Shuttle vector psw6 (BRBI-) BRIT BIO-TECHN LTD Shuttle vector pSW6 (first entry)

The vector is based on the 2u circle from S. cerevisiae deposited in S. cerevisiae strain BJ2168 as NCIMB 40326 shuttle vector capable of repleation in both E. coli and

It is a

Disclosure; Page 71; 115pp; English.

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cc shittle vector capable of replcation in both E. coli and S. cere-
cc visiae and contains origins of replication for both, the leu2 gene
(selectable marker), and an ampicillin resistant locus. The E. coli
csequences are derived from E. coli ColE1-based replicon pATI53. The
cvector contains an alpha factor pre-pro-peptide gene fused in frame
to the gene for epidermal growth factor (EGF). The expression of
this fusion is under control of a galactodse regulated promoter
chich contains hybrid DNA from S. cerevisiae GAL 1-10 promoter and
the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF
cgene can be excised by digestion with HindIII and BamHI. The plas-
c mid was used for the expression of a synthetic hirudin HV-1 gene
conservation vectors in which the hirudin gene is linked to a second
conservation of a sanother hirudin gene is linked to a second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residue Identity
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გგგგ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLP1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSW6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSW6
                                                                                                                                                                                                                       also contains the leu2 gene (a yeast selectable marker) and the amipicillin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced ability for passage through E.coli and this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha-factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under
                                                                                                                                                                                                                                                                                                                                                          on the 2 micron circle from Saccharomyces cerevisae. It is a shut vector capable of replication in both S. cerevisae and Escherichia coli as it contains the origin of replication for both organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New proteins comprising active protein and integrin-affinity sequence — are antithrombotics useful in treating and prevent myocardial infarction, stroke, pulmonary embolism and deep v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10; phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss.
                                       expression vector must therefore have the general composition: HindIII
                                                                                                                                                        the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dawson KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are released specifically at the place where clot formation
                       site-alpha-factor adapter-gene-BamHI site.
                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence given is the yeast expression vector pSW6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 67; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-0CT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9207874-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pSW6 expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q25185 standard; DNA; 7984
Q25185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1992.
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7859 BP; 2317 A; 1656 C; 1600
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  7984 BP;
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deep vein
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gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide link contains a cleavage site for e.g. factor X or thrombin which can be cleaved, releasing the individual proteins which have antithrombotic activity. The enzymes which cleave the fusion protein are present at the site of the target thrombus so the active agents

X 10 20 30 X GAAGTTCCTATACTTTCTAGAGAATAGGAACTT	CC are separated by 8 inderections. MB, in the Sequence of CC the FRT has only 12 base pairs on the 3' end of the spacer. The CC apparently missing base would be C. SQ Sequence 33 BP; 11 A; 5 C; 6 G; 11 T; Initial Score = 27 Optimized Score = 27 Significance = 7.58 Residue Identity = 81% Matches = 27 Mismatches = 6 Gaps = 0 Conservative Substitutions = 0	CC FIP recombinase is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy. CC number of the 2-mu plasmid of S. cerevisiae during DNA replication. CC The inventors claim a mammalian recombination system in which the CC FIP recombinase is pref. Q29101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair CC repeats, separated by an 8 base-pair spacer (see Q29100). The CC combination of nucleotides so long as the two 13 base-pair repeats of the spacer region can be replaced with any other CC combination of nucleotides so long as the two 13 base-pair repeats.	PF 06-MAR-1992; UO.8899. PR 08-MAR-1991; US.666253. PA (SAIK) SAIK INST BIOLOGICAL STUDIES. PI Ogorman SV, Wahl GM; DR WPI; 92-331739/40. PT precise modification by recombination and can be used to alter PT transgenee for therapeutic purposes and analysis of development PS Claim 33; Page 40; 49pp; English.		y Identity = 82% b 10 20 GAAGTTCCTATACTTCTAGAGA
Theria; Eutheria; Lagomorpha; Leporidae. REFERENCE 1 (bases 1 to 2157) AUTHORS Thomas,B. TITLE Direct Submission JOURNAL Submitted (04-JUL-1989) Thomas B., Swiss Federal Institute of Technologie Zuerich, C/O Dr K Buerki Preclinical Research Sandoz Ltd, 4002 Basel , Switzerland. STANDARD full automatic	OCCASB5 ON Rabbit DNA N X15735 N X15736 rabbit rabbit SM Oryctolagy Eukaryota;	X GAACTTCCTATACTTTCTAGAATAGGAACTTC	source 1.2415 ### Arm	IGCATION/Qualifiers 881278 /note="OFF1" /product="house-keeping protein" /codon start=1 /codon	MUSHKPRO MUSHKPRO MUSHKPRO ACCESSION ACCESSION MY4555 KEYWORDS SOURCE ORGANISM Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Murinae. REFERENCE AUTHORS MUSHKPRO 21-AUG-1991 21-AUG-1991 21-AUG-1991 21-AUG-1991 ACCESSION MUSHKPRO 21-AUG-1991 21-AUG-1991 ACCESSION MUSHKPRO 21-AUG-1991 ACCESSION MUSHKPRO ACCESSION ACCESSION MUSHKPRO ACCESSION MUSHKPRO ACCESSION MUSHKPRO ACCESSION ACCESSION ACCESSION ACCESSION MUSHKPRO ACCESSION ACCESSION ACCESSION MUSHKPRO ACCESSION ACCES

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8. FLP1' (1-34)
RSCALPST
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                                                                       STANDARD
REFERENCE
AUTHORS
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         2 (bases 1 to 1931)
1 Tahida, S., Emori, Y. and Suzuki, K.
Rat calpastatin has diverged primary sequence from other mammalian calpastatins but retains functionally important sequences
Biochim. Biophys. Acta 1088, 436-438 (1991)
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                                                                                                                    Submitted (12-NOV-1990) Y. Emori, BIOCHEMISTRY, FACULTY OF SCIENCE, BUNKYO-KU, TOKYO 113, JAPAN
                                                                                                                                                                                         Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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1 (bases 1 to 308)
Hatch, C.L. and Bonner, W.M.
The human histone H2a.z gene: Sequence and regulation
J. Biol. Chem. 265, 15211-15218 (1990)
                                                                                                                                                                                                                                                                                                    Human histone H2A.Z
L10137 M33917
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Gaps Initial Score = Residue Identity = Gaps = 10. FLP1' (1-34) Q23917 Initial Score in host cells

Claim 8; Page 6; 80pp; English.

Chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified

Chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified

Cwith degenerate primers corresponding to the amino acid sequences

of conserved regions of known thermostable polymerases. When

specific PCR products of a similar size to the product generated

cusing Tag chromosomal DNA were produced, the PCR fragments were

cloned and sequenced. Fragments with sequences which encoded

regions of amino acid homology to known thermostable polymerases

were identified. The cloned PCR products were used as probes to

screen a genomic Southern blot. The full-length Taf coding sequence

was then compiled from various clones. See also Q23918-Q23961.

Sequence 4286 BP; 1623 A; 470 C; 847 G; 1346 T; X 10 20 30 X GAAGTTCCTATACTTTCTAGAGAATAGGAACTTC Q23917 standard; DNA; 4286 BP.
Q23917;
27-QCT-1992 (first entry)
Taf DNA polymerase I coding sequence.
Thermostability; PCR; polymerase chain reaction;
thermophilic bacteria; Taf Pol I; ss. Thermostable DNA polymerase from Thermosipho africanus - prepd. by purificn. from cells or by expression of Taf polymerase gene (CETU) CETUS CORP.

Abramson RD, Gelfand DH, Greenfield L, Lawyer FC, Reichert FL; WPI; 92-150887/18. /product= Polymerase_I w09206202-A. P-PSDB; R23122. 26-SEP-1991; 28-SEP-1990; Thermosipho africanus. /*tag= Taf DNA polymerase I coding sequence. 007076. US-590490. 23 67**%** 0 Location/Qualifiers 298..2976 Conservative Substitutions Optimized Score = Matches = 23 Significance = 23 Mismatches =

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Set Description Items

Si 346 FLP (10N) RECOMBINAS? **S2** 124 RD (unique items)

?#223/1-124

2/3/1 (Item 1 from file: 155)

08080444 92218444

Reactions between half- and full-FLP recombination target sites. A model system for analyzing early steps in FLP protein-mediated site-specific recombination.

Qian XH; Inman RB; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706.

J Biol Chem (UNITED STATES) Apr 15 1992, 267 (11) p7794-805, ISSN 0021-9258 Journal Code: HIV

Contract/Grant No.: GM-32335; GM-14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

(Item 2 from file: 155) 5%3/5

07913378 92051378

GLP-mediated recombination in the vector mosquito, Aedes aegypti.

Morris AC; Schaub TL; James AA

Department of Molecular Biology & Biochemistry, University of California, Irvine 92717.

Nucleic Acids Res (ENGLAND) Nov 11 1991, 19 (21) p5895-900, ISSN 0305-1048 Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

(Item 3 from file: 155) 2/3/3

07823652 91342652

Synapsis, strand scission, and strand exchange induced by the FLP recombinase: analysis with half-FRT sites.

Amin A; Roca H; Luetke K; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

Mol Cell Biol Sep 1991, 11 (9) p4497-508, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/4 (Item 4 from file: 155)

07777737 91296737

Domain of a yeast site-specific recombinase (Flp) that recognizes its target site.

Chen JW; Evans BR; Yang SH; Teplow DB; Jayaram M

Department of Microbiology, University of Texas, Austin 78712.

Proc Natl Acad Sci U S A Jul 15 1991, 88 (14) p5944-8, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/5 (Item 5 from file: 155)

07731454 91250454

Identification of the DNA-binding domain of the FLP recombinase.

Pan H; Clary D; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Biol Chem Jun 15 1991, 266 (17) p11347-54, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/6 (Item 6 from file: 155)

07687992 91206992

Integration specificity of retrotransposons and retroviruses.

Sandmeyer SB; Hansen LJ; Chalker DL

Department of Microbiology and Molecular Genetics, College of Medicine, University of California, Irvine 92717.

Annu Rev Genet 1990, 24 p491-518, ISSN 0066-4197 Journal Code: 6DP

Contract/Grant No.: GM33281

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC

2/3/7 (Item 7 from file: 155)

07668658 91187658

A bacterial model system for chromosomal targeting.

Huang LC; Wood EA; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Nucleic Acids Res Feb 11 1991, 19 (3) p443-8, ISSN 0305-1048

Journal Code: O&L

Contract/Grant No.: GM37835

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/8 (Item 8 from file: 155)

07645850 91164850

Recombinase-mediated gene activation and site-specific integration in mammalian cells.

O'Gorman S; Fox DT; Wahl GM

Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

Science Mar 15 1991, 251 (4999) p1351-5, ISSN 0036-8075

Journal Code: UJ7

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/9 (Item 9 from file: 155)

07643634 91162634

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes. Differential activity in full-site and half-site recombinations.

Chen JW; Evans BR; Zheng L; Jayaram M

Department of Microbiology, University of Texas at Austin, Austin 78712.

J Mol Biol Mar 5 1991, 218 (1) p107-18, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/10 (Item 10 from file: 155)

07554393 91073393

FLP protein of 2 mu circle plasmid of yeast induces multiple bends in the FLP recognition target site.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1990, 216 (2) p289-98, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/11 (Item 11 from file: 155)

07553382 91072382

Protein-based asymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination.

Qian XH; Inman RB; Cox MM

Program in Cell and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706.

J Biol Chem Dec 15 1990, 265 (35) p21779-88, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM 37835; GM 14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/12 (Item 12 from file: 155)

07490349 91009349

Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination [published erratum appears in J Biol Chem 1991 Apr 15;266(11):7312]

Evans BR; Chen JW; Parsons RL; Bauer TK; Teplow DB; Jayaram M

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Oct 25 1990, 265 (30) p18504-10, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/13 (Item 13 from file: 155)

07410836 90317836

Synaptic intermediates promoted by the FLP recombinase.

Amin AA; Beatty LG; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Jul 5 1990, 214 (1) p55-72, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/14 (Item 14 from file: 155)

07263960 90170960

Functional analysis of Arg-308 mutants of Flp recombinase. Possible role of Arg-308 in coupling substrate binding to catalysis.

Parsons RL; Evans BR; Zheng L; Jayaram M

Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Mar 15 1990, 265 (8) p4527-33, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/15 (Item 15 from file: 155)

07229522 90136522

Use of site-specific recombination to regenerate selectable markers.

Cregg JM; Madden KR

Salk Institute Biotechnology/Industrial Associates, Inc., La Jolla, CA 92037.

Mol Gen Genet Oct 1989, 219 (1-2) p320-3, ISSN 0026-8925

Journal Code: NGP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/16 (Item 16 from file: 155)

07190832 90097832

Characterization of Holliday structures in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Inman RB; Cox MM

Program in Cellular and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Jan 1990, 10 (1) p235-42, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/17 (Item 17 from file: 155)

07123422 90030422

The FLP recombinase of yeast catalyzes site-specific recombination in the Drosophila genome.

Golic KG: Lindquist S

Howard Hughes Medical Institute, Department of Molecular Genetics and Cell Biology, University of Chicago, Illinois 60637.

Cell Nov 3 1989, 59 (3) p499-509, ISSN 0092-8674 Journal Code: CQ4 Contract/Grant No.: GM 25874

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/18 (Item 18 from file: 155)

07011744 89313744

Synthesis of an enzymatically active FLP recombinase in vitro: search for a DNA-binding domain.

Amin AA; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

Mol Cell Biol May 1989, 9 (5) p1987-95, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/19 (Item 19 from file: 155)

07002130 89304130

FLP-FRT mediated intrachromosomal recombination on a tandemly duplicated YEp integrant at the ILV2 locus of chromosome XIII in Saccharomyces cerevisiae.

Rank GH; Arndt GM; Xiao W

Department of Biology, University of Saskatchewan, Saskatoon, Canada.

Curr Genet Feb 1989, 15 (2) p107-12, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/20 (Item 20 from file: 155)

06876684 89178684

FLP recombinase of the 2 microns circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Feb 20 1989, 205 (4) p647-58, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/21 (Item 21 from file: 155)

06825220 89127220

Holliday intermediates and reaction by-products in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Huang LC; Umlauf SW; Cox MM; Inman RB

Department of Biochemistry, College of Agriculture and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Sep 1988, 8 (9) p3784-96, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/22 (Item 22 from file: 155)

06823587 89125587

The mechanism of loading of the FLP recombinase onto its DNA target sequence.

Beatty LG: Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1988, 204 (2) p283-94, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/23 (Item 23 from file: 155)

06794920 89096920

Step-arrest mutants of FLP recombinase: implications for the catalytic mechanism of DNA recombination.

Parsons RL; Prasad PV; Harshey RM; Jayaram M

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

Mol Cell Biol Aug 1988, 8 (8) p3303-10, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/24 (Item 24 from file: 155)

06761437 89063437

High frequency FLP-independent homologous DNA recombination of 2 mu plasmid in the yeast Saccharomyces cerevisiae.

Bruschi CV; Howe GA

Department of Microbiology and Immunology, School of Medicine, East Carolina University, Greenville, NC 27858-4354.

Curr Genet Sep 1988, 14 (3) p191-9, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/25 (Item 25 from file: 155)

06740094 89042094

Holliday junctions in FLP recombination: resolution by step-arrest mutants of FLP protein.

Jayaram M; Crain KL; Parsons RL; Harshey RM

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, CA 92037.

Proc Natl Acad Sci U S A Nov 1988, 85 (21) p7902-6, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/26 (Item 26 from file: 155)

06703077 89005077

The functional significance of DNA sequence structure in a site-specific genetic recombination reaction.

Umlauf SW; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

EMBO J Jun 1988, 7 (6) p1845-52, ISSN 0261-4189 Journal Code: EMB Contract/Grant No.: GM37835; AI00599; GM07215

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/27 (Item 27 from file: 155)

06687975 88332975

DNA recognition by the FLP recombinase of the yeast 2 mu plasmid. A mutational analysis of the FLP binding site.

Senecoff JF; Rossmeissl PJ; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

J Mol Biol May 20 1988, 201 (2) p405-21, ISSN 0022-2836

Journal Code: J6V

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/28 (Item 28 from file: 155)

06643050 88288050

Nucleotide sequencing and expression of the fadL gene involved in long-chain fatty acid transport in Escherichia coli.

Said B; Ghosn CR; Vu L; Nunn WD

Department of Molecular Biology and Biochemistry, University of California, Irvine 92717.

Mol Microbiol May 1988, 2 (3) p363-70, ISSN 0950-382X

Journal Code: MOM

Contract/Grant No.: GM 22466-11

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/29 (Item 29 from file: 155)

06618001 88263001

FLP recombinase is an enzyme.

Gates CA; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Proc Natl Acad Sci U S A Jul 1988, 85 (13) p4628-32, ISSN 0027-8424 Journal Code: PV3

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/30 (Item 30 from file: 155)

06567126 88212126

Mutations that improve the binding of yeast FLP recombinase to its \mathbb{R}^2 substrate.

Lebreton B; Prasad PV; Jayaram M; Youderian P

Department of Biological Sciences, University of Southern California, Los Angeles 90089-1481.

Genetics Mar 1988, 118 (3) p393-400, ISSN 0016-6731 Journal Code: FNH

Contract/Grant No.: GM34982; GM35654

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/31 (Item 31 from file: 155)

06521666 88166666

Antagonistic controls regulate copy number of the yeast 2 mu plasmid.

Murray JA; Scarpa M; Rossi N; Cesareni G

EMBL, Heidelberg, FRG.

EMBO J Dec 20 1987, 6 (13) p4205-12, ISSN 0261-4189 Journal Code: EMB

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/32 (Item 32 from file: 155)

06506025 88151025

Autoregulation of 2 micron circle gene expression provides a model for

maintenance of stable plasmid copy levels.

Som T; Armstrong KA; Volkert FC; Broach JR

Department of Molecular Biology, Princeton University, New Jersey 08544.

Cell Jan 15 1988, 52 (1) p27-37, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/33 (Item 33 from file: 155)

06342913 87316913

Purification of the FLP site-specific recombinase by affinity chromatography and re-examination of basic properties of the system.

Meyer-Leon L; Gates CA; Attwood JM; Wood EA; Cox MM

Nucleic Acids Res Aug 25 1987, 15 (16) p6469-88, ISSN 0305-1048

Journal Code: O&L

Contract/Grant No.: GM32335; GM37835; AI00599; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/34 (Item 34 from file: 155)

06280212 87254212

Isolation of intermediates in the binding of the FLP recombinase of the yeast plasmid 2-micron circle to its target sequence.

Andrews BJ; Beatty LG; Sadowski PD

J Mol Biol Jan 20 1987, 193 (2) p345-58, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/35 (Item 35 from file: 155)

06274060 87248060

Rapid localization and characterization of random mutations within the 2 micron circle site-specific recombinase: a general strategy for analysis of protein function [published erratum appears in Gene 1987:57(1):149]

Govind NS; Jayaram M

Gene 1987, 51 (1) p31-41, ISSN 0378-1119 Journal Code: FOP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/36 (Item 36 from file: 155)

06210407 87184407

Site-specific recombination of the yeast plasmid two-micron circle: intermediates in the binding process.

Andrews BJ; Beatty LG; Sadowski PD

Basic Life Sci 1986, 40 p407-24, ISSN 0090-5542 Journal Code: 9K0

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/37 (Item 37 from file: 155)

06210406 87184406

Site-specific recombination promoted in vitro by the FLP protein of the yeast two-micron plasmid.

Senecoff JF; Bruckner RC; Meyer-Leon L; Gates CA; Wood E; Umlauf SW; Attwood JM; Cox MM

Basic Life Sci 1986, 40 p397-405, ISSN 0090-5542 Journal Code: 9K0

Contract/Grant No.: GM32335; 5-T32 GM07215; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/38 (Item 38 from file: 155)

06210404 87184404

Survival strategies of the yeast plasmid two-micron circle.

Volkert FC; Wu LC; Fisher PA; Broach JR

Basic Life Sci 1986, 40 p375-96, ISSN 0090-5542 Journal Code: 9K0

Contract/Grant No.: GM34596; GM33132

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/39 (Item 39 from file: 155)

06201639 87175639

Mutations in the 2-microns circle site-specific recombinase that abolish recombination without affecting substrate recognition [published erratum appears in Proc Natl Acad Sci U S A 1988 Mar;85(5):1497]

Prasad PV; Young LJ; Jayaram M

Proc Natl Acad Sci U S A Apr 1987, 84 (8) p2189-93, ISSN 0027-8424

Journal Code: PV3 Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/40 (Item 40 from file: 155)

06167165 87141165

Association of reciprocal exchange with gene conversion between the repeated segments of 2-micron circle.

Jayaram M

J Mol Biol Oct 5 1986, 191 (3) p341-54, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/41 (Item 41 from file: 155)

06115790 87089790

Substrate recognition by the 2 micron circle site-specific recombinase: effect of mutations within the symmetry elements of the minimal substrate.

Prasad PV; Horensky D; Young LJ; Jayaram M

Mol Cell Biol Dec 1986, 6 (12) p4329-34, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM 35654-01

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/42 (Item 42 from file: 155)

06115725 87089725

Mating type-like conversion promoted by the 2 micrograms circle site-specific recombinase: implications for the double-strand-gap repair model.

Jayaram M

Mol Cell Biol Nov 1986, 6 (11) p3831-7, ISSN 0270-7306 Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/43 (Item 43 from file: 155)

06115667 87089667

Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 microns circle.

McLeod M; Craft S; Broach JR

Mol Cell Biol Oct 1986, 6 (10) p3357-67, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/44 (Item 44 from file: 155)

06090546 87064546

Interaction of the FLP recombinase of the Saccharomyces cerevisiae 2 micron plasmid with mutated target sequences.

Andrews BJ; McLeod M; Broach J; Sadowski PD

Mol Cell Biol Jul 1986, 6 (7) p2482-9, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/45 (Item 45 from file: 155)

06009798 86310798

The FLP recombinase of the Saccharomyces cerevisiae 2 microns plasmid attaches covalently to DNA via a phosphotyrosyl linkage.

Gronostajski RM: Sadowski PD

Mol Cell Biol Nov 1985, 5 (11) p3274-9, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/46 (Item 46 from file: 155)

06003314 86304314

Specific contacts between the FLP protein of the yeast 2-micron plasmid and its recombination site.

Bruckner RC; Cox MM

J Biol Chem Sep 5 1986, 261 (25) p11798-807, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/47 (Item 47 from file: 155)

05983659 86284659

Chromatin organization of the Saccharomyces cerevisiae 2 microns plasmid depends on plasmid-encoded products.

Veit BE; Fangman WL

Mol Cell Biol Sep 1985, 5 (9) p2190-6, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM18926

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/48 (Item 48 from file: 155)

05980709 86281709

FLP site-specific recombinase of yeast 2-micron plasmid. Topological features of the reaction.

Beatty LG; Babineau-Clary D; Hogrefe C; Sadowski PD

J Mol Biol Apr 20 1986, 188 (4) p529-44, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/49 (Item 49 from file: 155)

05971102 86272102

Site-specific recombination promotes plasmid amplification in yeast.

Volkert FC; Broach JR

Cell Aug 15 1986, 46 (4) p541-50, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM-34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/50 (Item 50 from file: 155)

05958059 86259059

The minimal duplex DNA sequence required for site-specific recombination promoted by the FLP protein of yeast in vitro.

Proteau G; Sidenberg D; Sadowski P

Nucleic Acids Res Jun 25 1986, 14 (12) p4787-832, ISSN 0305-1048

Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/51 (Item 51 from file: 155)

05931585 86232585

Sequence organization of the circular plasmid pKD1 from the yeast Kluyveromyces drosophilarum.

Chen XJ; Saliola M; Falcone C; Bianchi MM; Fukuhara H

Nucleic Acids Res Jun 11 1986, 14 (11) p4471-81, ISSN 0305-1048

Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/52 (Item 52 from file: 155)

05923006 86224006

Directionality in FLP protein-promoted site-specific recombination is mediated by DNA-DNA pairing.

Senecoff JF; Cox MM

J Biol Chem Jun 5 1986, 261 (16) p7380-6, ISS \ 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/53 (Item 53 from file: 155)

05919123 86220123

The integrase family of site-specific recombinase; regional similarities

and global diversity. Argos P; Landy A; Abremski K; Egan JB; Haggard Ljungquist E; Hoess RH; Kahn ML; Kalionis B; Narayana SV; Pierson LS 3d; et al EMBO J Feb 1986, 5 (2) p433-40, ISSN 0261-418) Journal Code: EMB Contract/Grant No.: AI 13544 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/54 (Item 54 from file: 155) 05810590 86111590 Site-specific recombinases: changing partners and doing the twist. Sadowski P J Bacteriol Feb 1986, 165 (2) p341-7, ISSN 0321-9193 Journal Code: **HH3** Languages: ENGLISH Document type: JOURNAL ARTICLE; REVIEW 2/3/55 (Item 55 from file: 155) 05741647 86042647 The FLP recombinase of the yeast 2-micron plasmid: characterization of its recombination site. Senecoff JF; Bruckner RC; Cox MM Proc Natl Acad Sci U S A Nov 1985, 82 (21) p72/0-4, ISSN 0027-8424 Journal Code: PV3 Contract/Grant No.: GM32335 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/56 (Item 56 from file: 155) 05707309 86008309 protein The FLP of the 2-micron plasmid of yeast. Interintramolecular reactions. Gronostajski RM; Sadowski PD J Biol Chem Oct 5 1985, 260 (22) p12328-35, IBSN 0021-9258 Journal Code: HIV Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/57 (Item 57 from file: 155) 05707308 86008308 Determination of DNA sequences essential for FL :-mediated recombination by a novel method. Gronostajski RM; Sadowski PD J Biol Chem Oct 5 1985, 260 (22) p12320-7, ISBN 0021-9258 Journal Code: HIV Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/58 (Item 58 from file: 155) 05707307 86008307 The FLP protein of the 2-micron plasmid of yeast. Purification of the protein from Escherichia coli cells expressing the :loned FLP gene. Babineau D; Vetter D; Andrews BJ; Gronostajski RM; Proteau GA; Beatty LG;

Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12313-9, ISSN 0021-9258 Journal Code: HIV Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/59 (Item 59 from file: 155) 05560933 85176933 The FLP recombinase of the 2 micron circle DNA of yeast: interaction with its target sequences. Andrews BJ; Proteau GA; Reatty LG; Sadowski PD Apr 1985, 40 (4) p795-803, ISSN 0092-8674 Journal Code: CQ4 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/60 . (Item 1 from file: 5) 8906509 _ BIOSIS Number: 42131509 AN ORDERED DISASSEMBLY OF COMPLEXES OF FLP RECOMBINASE AND FRT SITES FOLLOWING RECOMBINATION WAITE L L; COX M M DEP. BIOCHEM., UNIV. WISCONSTN, MADISON, WIS. 53706. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNG REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANDARY 25-FI BRUARY 1. 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 67. CODEN: J(BSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/61 (Item 2 from file: 5) 8906501 BIOSIS Number: 42131501 LIGATION ACTIVITY OF THE FLP RECOMBINASE PAN G; SADOWSKI P D DEP. MOLECULAR MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNF REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FIBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 65. CODEN: J(BSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/62 (Item 3 from file: 5) 8906498 BIOSIS Number: 42131498 HALF-SITE RECOMBINATIONS MEDIATED BY FLP RECOMBINASE FROM SACCHAROMYCES-CEREVISIAE SERRE M-C; LEI-ZHENG; JAYARAM M DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78746. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNF REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 64. CODEN: J(BSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/63 (Item 4 from file: 5)

BIOSIS Number: 42131492

FUNCTIONAL ANALYSES OF MUTANTS OF FLP AND R RECOMBINASE FROM YEAST CHEN J-W; LEE J; EVANS B; SERRE M-C; ARAKI H; OSPIMA Y; JAYARAM M

DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND

RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL
BIOCHEM SUPPL 0 (16 PART B). 1992. 62. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/64 (Item 5 from file: 5)

8197568 BIOSIS Number: 91118568

TYROSINE-60 VARIANTS OF FLP RECOMBINASE GENERATE CONFORMATIONALLY ALTERED PROTEIN DNA COMPLEXES DIFFERENTIAL ACTIVITY IN FULL-SITE AND HALF RECOMBINATIONS

CHEN J-W; EVANS B R; ZHENG L; JAYARAM M

DEP. MICRBOIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712, USA.

J MOL BIOL 218 (1). 1991. 107-118. CODEN: JMORA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/65 (Item 6 from file: 5)

7103760 BIOSIS Number: 88026505

FLP-FRT MEDIATED INTRACHROMOSOMAL RECOMBINATION ON A TANDEMLY DUPLICATED YE-P INTEGRANT AT THE ILV2 LOCUS OF CHROMOSOME XIII IN SACCHAROMYCES-CEREVISIAE

RANK G H; ARNDT G M; XIAO W

DEP. BIOL., UNIV. SASKATCHEWAN, SASKATOON, SASKATCHEWAN, CANADA S7N 0W0. CURR GENET 15 (2). 1989. 107-112. CODEN: CUGED

Full Journal Title: Current Genetics

Language: ENGLISH

2/3/66 (Item 7 from file: 5)

7043154 BIOSIS Number: 87103675

FLP RECOMBINASE OF THE 2 MUM CIRCLE PLASMID OF SACCHAROMYCES-CEREVISIAE BENDS ITS DNA TARGET ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BENDING SCHWARTZ C J E; SADOWSKI P D

DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN.

J MOL BIOL 205 (4). 1989. 647-658. CODEN: JMOBA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/67 (Item 8 from file: 5)

6944460 BIOSIS Number: 87004981

HIGH FREQUENCY FLP-INDEPENDENT HOMOLOGOUS DNA RECOMBINATION OF 2 MICRON PLASMID IN THE YEAST SACCHAROMYCES-CEREVISIAE

BRUSCHI C V: HOWE G A

DEP. MICROBIOL. IMMUNOL., SCH. MED., EAST CAROLINA UNIV., GREENVILLE, N.C. 27858-4354, U.S.A.

CURR GENET 14 (3). 1988. 191-200. CODEN: CUGED

Full Journal Title: Current Genetics

Language: ENGLISH

2/3/68 (Item 9 from file: 5)

6892306 BIOSIS Number: 37086685

THE FLP RECOMBINASE STEP-ARREST MUTANTS AND INTERMEDIATES IN RECOMBINATION

JAYARAM M; PARSONS R; EVANS B

RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037.

SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA R PLICATION AND RECOMBINATION HELD AT THE 18TH ANNUAL UCLA (UNIVERSITY OF ALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, TEAMBOAT SPRINGS, COLORADO, USA, MARCH 27-APRIL 3, 1989. J CELL BIOCHEM UPPL Ø (13 PART D). 1989. 106. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/69 (Item 10 from file: 5)

6636107 BIOSIS Number: 86102658

AUTOREGULATION OF 2-MUM CIRCLE GENE EXPRES ION PROVIDES A MODEL FOR MAINTENANCE OF STABLE PLASMID COPY LEVELS

SOM T; ARMSTRONG K A; VOLKERT F C; BROACH J R

DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, NEW JERSEY 08544.

CELL 52 (1). 1988. 27-38. CODEN: CELLB

Full Journal Title: Cell

Language: ENGLISH

2/3/70 (Item 11 from file: 5)

6624830 BIOSIS Number: 86091381

THE INT FAMILY OF SITE-SPECIFIC RECOMBINASES SOME THOUGHTS ON A GENERAL REACTION MECHANISM

JAYARAM M

DEP. MOL. BIOL., RES. INST. SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J GENET 67 (1). 1988. 29-36. CODEN: JOGIA

Full Journal Title: Journal of Genetics

Language: ENGLISH

2/3/71 (Item 12 from file: 5)

6571174 BIOSIS Number: 86037725

FLP RECOMBINASE INDUCTION OF THE BREAKAGE-FUSION-BRIDGE CYCLE AND GENE CONVERSION IN SACCHAROMYCES-CEREVISIAE

RANK G H; XIAO W; KOLENOVSKY A; ARNDT G

DEP. BIOL., UNIV. SASK., SASKATOON, SASK., CAN. S7N OWO.

CURR GENET 13 (4). 1988. 273-282. CODEN: CUGED

Full Journal Title: Current Genetics

Language: ENGLISH

2/3/72 (Item 13 from file: 5)

6150196 BIOSIS Number: 35015717

PURIFICATION OF FLP RECOMBINASE USING SEQUENCE-SPECIFIC DNA AFFINITY CHROMATOGRAPHY

GATES C A; MEYER-LEON L; ATTWOOD J M; WOOD E A; COX M M

DEP. BIOCHEM., UNIV. WIS.-MADISON, MADISON, WIS. 53706, USA.

BURGESS, R. (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 68. PROTEIN PURIFICATION: MICRO TO MACRO; CETUS-UCLA SYMFOSIUM, FRISCO, COLORADO, USA, MARCH 29-APRIL 4, 1987. XVIII+510P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2667-9. 0 (0). 1987. 197-206. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/73 (Item 14 from file: 5)

5802738 BIOSIS Number: 83065045

SUBSTRATE RECOGNITION BY THE 2-MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE EFFECT OF MUTATIONS WITHIN THE SYMMETRY ELEMENTS OF THE MINIMAL SUBSTRATE

PRASAD P V; HORENSKY D; YOUNG L-J; JAYARAM M

DEP. MOL. BIOL., RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037, USA.

MOL CELL BIOL 6 (12). 1986. 4329-4334. CODEN: MCEBD

Full Journal Title: Molecular and Cellular Biology

Language: ENGLISH

2/3/74 (Item 15 from file: 5)

5761770 BIOSIS Number: 83024077

MATING TYPE-LIKE CONVERSION PROMOTED BY THE 2 MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE IMPLICATIONS FOR THE 'DOUBLE-STRAND-GAP REPAIR MODEL

JAYARAM M

DEP. MOLECULAR BIOLOGY, RESEARCH INST. SCRIPPS CLINIC, LA JOLLA, CALIFORNIA 92037.

MOL CELL BIOL 6 (11). 1986. 3831-3837. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/75 (Item 16 from file: 5)

5751545 BIOSIS Number: 83013852

ASSOCIATION OF RECIPROCAL EXCHANGE WITH GENE CONVERSION BETWEEN THE REPEATED SEGMENTS OF 2-MICROMETER CIRCLE

JAYARAM M

DEPARTMENT OF MOLECULAR BIOLOGY, RESEARCH INSTITUTE OF SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J MOL BIOL 191 (3). 1986. 341-354. CODEN: JMOBA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/76 (Item 17 from file: 5)

5696494 RIOSIS Number: 33091515

MECHANISMS OF ACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; BEATTY L G; CLARY D; OLLERHEAD S

DEP. MED. GENETICS, MED. SCIENCES BUILD., UNIV. TORONTO, TORONTO, CANADA M5S 1A8.

MCMACKEN, R. AND T. J. KELLY (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 47. DNA REPLICATION AND RECOMBINATION; PARK CITY, UTAH, USA, MARCH 16-23, 1986. XXVI+782P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2646-6. 0 (0). 1987. 691-702. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/77 (Item 18 from file: 5) 5504855 BIOSIS Number: 32027162

INTERACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID WITH ITS TARGET SEQUENCE

SADOWSKI P D; ANDREWS B J; BEATTY L G; SIDENBERG D; PROTEAU G DEP. MED. GENETICS, UNIV. TORONTO, TORONTO M5S 1A8, CAN.

KLAR, A. AND J. N. STRATHERN (ED.). CURRENT COMMUNICATIONS IN MOLECULAR BIOLOGY: MECHANISMS OF YEAST RECOMBINATION; MEETING, COLD SPRING HARBOR, N.Y., USA. IX+193P. COLD SPRING HARBOR LABORATORY: COLD SPRING HARBOR, N.Y., USA. ILLUS. PAPER. ISBN 0-87969-195-6. 0 (0). 1986. 7-10. CODEN: 24607

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/78 (Item 19 from file: 5)

5426144 BIOSIS Number: 82070947

INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID WITH MUTATED TARGET SEQUENCES

ANDREWS B J; MCLEOD M; BROACH J; SADOWSKI P D

DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO, ONTARIO M5S 1A8, CANADA.

MOL CELL BIOL 6 (7). 1986. 2482-2489. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/79 (Item 20 from file: 5) 5389362 BIOSIS Number: 82034165

FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MICROMETER PLASMID TOPOLOGICAL FEATURES OF THE REACTION

BEATTY L G; BABINEAU-CLARY D; HOGREFE C; SADOWSKI P D

DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO M5S 1A8, CANADA.

J MOL BIOL 188 (4). 1986. 529-544. CODEN: JMOBA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/80 (Item 21 from file: 5)

5265813 BIOSIS Number: 81033120

THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

GRONOSTAJSKI R M; SADOWSKI P D

DEP. MED. GENET., UNIV. TORONTO, TORONTO, ONT. M5S1A8, CHN.

MOL CELL BIOL 5 (11). 1985. 3274-3279. CODEN: MCEBD

Full Journal Title: Molecular and Cellular Biology

Language: ENGLISH

2/3/81 (Item 22 from file: 5)

5256098 BIOSIS Number: 81023405

THE FLP PROTEIN OF THE 2-MICRON PLASMID OF YEAST SACCHAR MYCES-CEREVISIAE PURIFICATION OF THE PROTEIN FROM ESCHERICHIA-COLI CELLS EX! RESSING THE CLONED FLP GENE

BABINEAU D; VETTER D; ANDREWS B J; GRONOSTAJSKI R M; PROTEAU G A; BEATTY L G; SADOWSKI P D

DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, MSS 1A8, CANEDA. J BIOL CHEM 260 (22). 1985. 12313-12319. CODEN: JBCHA

Full Journal Title: Journal of Biological Chemistry

Language: ENGLISH

2/3/82 (Item 23 from file: 5)

5168213 BIOSIS Number: 31057528

THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; ANDREWS B J; BABINEAU-CLARY D; BEATTY L; GRONOSTAJSKI R M; PROTEAU G; SIDENBERG D

DEF. MED. GENET., UNIV. TORONTO, TORONTO M5S 1A8, CANADA.

SYMPOSIUM ON MECHANISMS OF DNA REPLICATION AND RECOMBINATION HELD AT THE 15TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, MAR. 16-23, 1986. J CELL BIOCHEM SUPPL Ø (10 PART B). 1986. 137. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/83 (Item 24 from file: 5) 4696890 BIOSIS Number: 29054205

INTERACTION OF THE FLP RECOMBINASE WITH SUBSTRATE 2-MICRON CIRCLE DNA ANDREWS B J; BEATTY L; SADOWSKI P D UNIV. TORONTO.

SYMPOSIUM ON YEAST CELL BIOLOGY HELD AT THE 14TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA - LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, APR. 9-15, 1985. J CELL BIOCHEM SUPPL Ø (9 PART C). 1985. 117. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/84 (Item 1 from file: 399)

116167825 CA: 116(17)167825y PATENT

Methods for in vitro recombination of multigene families for generation of new phenotypes

INVENTOR (AUTHOR): Short, Jay M.; Sorge, Joseph A.

LOCATION: USA

ASSIGNEE: Stratagene

PATENT: PCT International; WO 9116427 A1 DATE: 911031 APPLICATION: WO 91US2910 (910424) *US 513957 (900424)

FAGES: 204 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/00A; C12P-019734B; C12P-021/06B; C07H-021/00B DESIGNATED COUNTRIES: AU; CA; FI; JP; KR; NO DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE

Copyright 1992 by the American Chemical Society

2/3/85 (Item 2 from file: 399)

106208826 CA: 106(25)208826p JOURNAL

Rapid localization and characterization of random mutations within the 2.mu. circle site-specific recombinase: a general strategy for analysis of protein function

AUTHOR(S): Govind, Nadathur S.; Jayaram, Makkuni

LOCATION: Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA

JOURNAL: Gene DATE: 1987 VOLUME: 51 NUMBER: 1 PAGES: 31-41 CODEN: GENED6 ISSN: 0378-1119 LANGUAGE: English

Copyright 1992 by the American Chemical Society

2/3/86 (Item 3 from file: 399)

104001445 CA: 104(1)1445b JOURNAL

The FLP recombinase of the yeast 2-.mu.m plasmid: characterization of its recombination site AUTHOR(S): Senecoff, Julie F.; Bruckner, Robert C.; Cox, Michael M. LOCATION: Coll. Agric. Life Sci., Univ. Wisconsin, Madison, WI, 53706. JOURNAL: Proc. Natl. Acad. Sci. U. S. A. DATE: 1985 VOLUME: 82 NUMBER: 21 PAGES: 7270-4 CODEN: PNASA6 ISSN: 0027-8424 LANGUAGE: English Copyright 1992 by the American Chemical Society 2/3/87 (Item 4 from file: 399) 102216080 CA: 102(25)216080y JOURNAL The FLP recombinase of the 2.mu. circle DNA of yeast: interaction with its target sequences AUTHOR(S): Andrews, Brenda J.; Proteau, Gerald A.; Beatty, Linda G.; Sadowski, Paul D. LOCATION: Dep. Med. Genet., Univ. Toronto, Toronto, ON, Can., M5S 1A8 JOURNAL: Cell (Cambridge, Mass.) DATE: 1985 VOLUME: 40 NUMBER: 4 PAGES: 795-803 CODEN: CELLES ISSN: 0092-8674 LANGUAGE: English Copyright 1992 by the American Chemical Society 2/3/88 (Item 1 from #11e: 434) 11506141 Genuine Article#: HN234 No. References: 35 Title: SITE-SPECIFIC RECOMBINATION OF 2-MU-M PLASMID OF YEAST SACCHAROMYRES-CEREVISIAE Author(s): FUSHNOVA EA Corporate Source: ST PETERBURG PEDIAT MED INST/ST PETERBURG//USSR/ Journal: GENETIKA, 1992, V28, N2 (FEB), P25-34 Language: RUSSIAN Document Type: ARTICLE (Abstract Available) 2/3/89 (Item 2 from file: 434) 11487805 Genuine Article#: HM053 No. References: 33 Title: SITE-SPECIFIC INTEGRATION OF THE HAEMOPHILUS-INFLUENZAE BACTERIOPHAGE HP1 - IDENTIFICATION OF THE POINTS OF RECOMBINATIONAL STRAND EXCHANGE AND THE LIMITS OF THE HOST ATTACHMENT SITE Author(s): HAUSER MA; SCOCCA JJ Corporate Source: JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205; JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205 Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N10 (APR 5), P 6859-6864 Language: ENGLISH Document Type: ARTICLE (Abstract Available) (Item 3 from file: 434) 2/3/90 11338662 Genuine Article#: HB304 / No. References: 21 Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM Author(s): BAYLEY CC; MORGAN JX; DALE EC; OW DW Corporate Source: USDA ARS, ETR PLANT GENE EXPRESS, 800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS, CTR PLANT GENE EXPRESS, 800 BUCHANAN

ST/ALBANY//CA/9471/8; UNIV CALIF BERKELEY, DEPT PLANT

PATHOL/BERKELEY/CA/94720

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/91 (Item 4 from file: 434) 11317754 Genuine Article#: GZ516 No. References: 33 Title: A FROG VIRUS-3 GENE CODES FOR A PROTEIN CONTAINING THE MOTIF CHARACTERISTIC OF THE INT FAMILY OF INTEGRASES Author(s): ROHOZINSKI J; GOORHA R Corporate Source: ST JUDE CHILDRENS HOSP, DEPT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101; ST JUDE CHILDRENS HOSP, DEPT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101 Journal: VIROLOGY, 1992, V186, N2 (FEB), P693-700 Language: ENGLISH Document Type: ARTICLE (Item 5 from file: 434) 2/3/92 10583597 Genuine Article## EP811 No. References: 61 Title: A NOVEL RECOMBINATOR IN YEAST BASED ON GENE-II PROTEIN FROM BACTERIOPHAGE-F1 Author(s): STRATHERN JN; WEINSTOCK KG; HIGGINS DR; MCGILL CR Corporate Source: NCI, FREDERICK CANC RES & DEV CTR. BASIC RES PROGRAM/FREDERICK//MD/21701 Journal: GENETICS, 1991, V127, N1, P61-73 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/93 (Item 6 from file: 434) 09323349 Genuine Article#: T4208 No. References: 45 Title: FLP RECOMBINASE OF THE 2-MU-M CIRCLE PLASMID OF SACCHAROMYCES-CEREVISIAE BENDS ITS DNA TARGET - ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BENDING Author(s): SCHWARTZ CJE; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1989, V205, N4, P647-658 Language: ENGLISH Document Type: ARTICLE 2/3/94 (Item 7 from file: 434) 07863892 Genuine Article#: F8861 No. References: 37 Title: ISOLATION OF INTERMEDIATES IN THE BINDING OF THE FLP RECOMBINASE OF THE YEAST PLASMID 2-MIRON CIRCLE TO ITS TARGET SEQUENCE Author(s): ANDREWS BJ; BEATTY LG; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1987, V193, N2, P345-358 Language: ENGLISH Document Type: ARTICLE (Item 8 from file: 434) 2/3/95 07372665 Genuine Article#: C9356 No. References: 23 Title: INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M PLASMID WITH MUTATED TARGET SEQUENCES Author(s): ANDREWS BJ; MCLEOD M; BROACH J; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/; COLD SPRING HARBOR LAB/COLD SPRING

Journal: MOLECULAR AND CELLULAR BIOLOGY, 1986, V6, N7, P2482-2489

HARBOR//NY/11724; PRINCETON UNIV, DEPT MOLEC BIOL/PRINCETON//NJ/08544

Language: ENGLISH Document Type: ARTICLE

2/3/96 (Item 9 from file: 434)

07260459 Genuine Article#: C1205 No. References: 44

Title: FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MU-M PLASMID - TOPOLOGICAL FEATURES OF THE REACTION

Author(s): BEATTY LG; BABINEAUCLARY D; HOGREFE C; SADOWSKI PD

Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1986, V188, N4, P529-544

Language: ENGLISH Document Type: ARTICLE

2/3/97 (Item 10 from file: 434)

06806789 Genuine Article#: AUF29 No. References: 22

Title: THE FLP RECOMBINASE OF THE YEAST 2-MU-M PLASMID - CHARACTERIZATION OF ITS RECOMBINATION SITE

Author(s): SENECOFF JF; BRUCKNER RC; COX MM

Corporate Source: UNIV WISCONSIN, COLL AGR & LIFE SCI, DEPT BIOCHEM, 420 HENRY MALL/MADISON//WI/53706

Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 1985, V82, N21, P7270-7274

Language: ENGLISH Document Type: ARTICLE

2/3/98 (Item 11 from file: 434)

06780315 Genuine Article#: ATE60 No. References: 28

Title: THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

Author(s): GRONOSTAJSKI RM: SADOWSKI PD

Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/

Journal: MOLECULAR AND CELLULAR BIOLOGY, 1985, V5, N11, P3274-3279

Language: ENGLISH Document Type: ARTICLE

2/3/99 (Item 1 from file: 76)

1171271 82001618771

Mutations in the 2-.mu.m circle site-specific recombinase that abolish recombination without affecting substrate recognition.

Prasad, P.V.; Young, L.-J.; Jayaram, M.

Dep. Mol. Biol., Res. Inst. Scripps Clin., 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

PROC. NATL. ACAD. SCI. USA; 84(8), pp. 2189-2193 1987

Language: English Summary Language: English

2/3/100 (Item 1 from file: 73)

8210454 EMBASE No: 91239554

Erratum: Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination (Vol. 265 (1990) 18504-18510)

Evans B.R.; Chen J.-W.; Parsons R.L.; Bauer T.K.; Teplow D.B.; Jayaram M. J. BIOL. CHEM. (USA), 1991, 266/11 (7312) CODEN: JBCHA ISSN: 0021-9258

LANGUAGES: English

2/3/101 (Item 2 from file: 73)

7363228 EMBASE No: 89079376

FLP recombinase of the 2 microm circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending

Schwartz C.J.E.; Sadowski P.D.

Department of Medical Genetics, University of Toronto, Toronto, Ont. M5S 1AB Canada

J. MOL. BIOL. (United Kingdom) , 1989, 205/4 (647-658) CODEN: JMOBA ISSN: 0022-2836

LANGUAGES: English

2/3/102 (Item 1 from file: 144) 09775158 PASCAL No.: 91-0572331

Domain of a yeast site-specific recombinase (Flp) that recognizes its target site

JING-WEN CHEN; EVANS B R; SANG-HWA YANG; TEPLOW D/ B; JAYARAM M Univ. Texas, dep. microbiology, Austin TX 78712, USA

Journal: Proceedings of the National Academy of Sciences of the United States of America, 1991, 88 (14) 5944-5948

Language: English

2/3/103 (Item 2 from file: 144)

09771721 PASCAL No.: 91-0568894

Protein-based assymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination

XIAO-HONG QIAN; INMAN R B; COX M M

Univ. Wisconsin, coll. agricultural life sci., dep. biochemistry, Madison WI 53706, USA

Journal: Journal of biological chemistry (The), 1990, 265 (35) 21779-21788

Language: English

2/3/104 (Item 3 from file: 144)

09730857 PASCAL No.: 91-0527991

Site-specific recombination between homologous chromosomes in Drosophila GOLIC K G

Univ. Chicago, Howard Hughes medical inst., dep; molcular genetics cell biology, Chicago IL 60637, USA

Journal: Science: (Washington, DC), 1991, 252 (5008) 958-961 Language: English

2/3/105 (Item 4 from file: 144)

09563896 PASCAL No.: 91-0354326

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes : differential activity in full-site and half-site recombinations $\frac{1}{2}$

JING-WEN CHEN; EVANS B R; LEI ZHENG; JAYARAM M Univ. Texas at Austin, dep. microbiology, Austin TX 78712, USA Journal: Journal of molecular biology, 1991, 218 (1) 107-118 Language: English

2/3/106 (Item 5 from file: 144) 07823248 PASCAL No.: 87-0302971

Interaction of the FLP recombinase of the saccharomyces cerevisiae 2 mu m

plasmid with mutated target sequences

NDREWS B J; MCLEOD M; BROACH J; SADOWSKI P D

Univ. Toronto, dep. medical genetics, Toronto ON M5S 1A8, Canada

Journal: Molecular and cellular biology, 1986, 6 (7) 2482-2489

Language: ENGLISH

2/3/107 (Item 1 from file: 77)

89015048 V17N02

FLP recombinase induction of the breakage-fusion-bridge cycle (BFBC) and gene conversion in Saccharomyces cerevisiae

Rank, G.H.; Xiao, W.; Kolenovsky, A.; Arndt, G.

Univ. Saskatchewan, Saskatoon, Sask., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/108 (Item 2 from file: 77)

89014585 V17N02

Structure-function relationship of the sequence specific DNA binding function of the FLP recombinase

Amin, A.A.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/109 (Item 3 from file: 77)

89014584 V17N02

FLP recombinase of 2 mu circle of S. cerevisiae bends its DNA target: An in vitro analysis

Schwartz, C.J.E.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/110 (Item 4 from file: 77)

89013277 V17N02

Mutational analysis of the FLP site-specific recombinase of the yeast 2 micron plasmid

Sadowski, P.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal

Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome

2/3/111 (Item 5 from file: 77)

89012894 V17N02

Step-arrest mutants of FLP recombinase: Implications for the mechanism of recombination

Evans, B.R.; Parsons, R.; Crain, K.; Jayaram, M.

Mol. Biol. Dep., Res. Inst. Scripps Clin. and Res. Found., La Jolla, CA, USA

14th International Conference on Yeast Genetics and Molecular Biology 8830578 Espoo (Finland) 7-13 Aug 1988

European Association for Cancer Research

Subscription Department C, John Wiley & Sons Inc., 605 Third Avenue, New York, NY 10158 (USA), Abstracts will be Published in Special Issue of Journal 'Yeast' Volume 4. ISSN 0749-503X

2/3/112 (Item 1 from file: 265)

0129563 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS

IDENTIFYING NO.: 5R01HG00250-04 AGENCY CODE: CRISP

Directed rearrangement of the mammalian genome in vivo

PRINCIPAL INVESTIGATOR: YOUDERIAN, PHILIP A

ADDRESS: CALIF INST OF BIOLOG RESEARCH 11099 NORTH TORREY PINES ROAD LA JOLLA, CA 92037

PERFORMING ORG.: CALIFORNIA INSTITUTE OF BIOLOGICAL RES, SAN DIEGO, CALIFORNIA

SPONSORING ORG.: NATIONAL CENTER FOR HUMAN GENOME RESEARCH FY: 92 FUNDS: \$182,972

2/3/113 (Ntem 2 from file: 265)

0127425 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 50016M35654-07 AGENCY CODE: CRISP Site specific recombination in the yeast plasmid 2 micron circle PRINCIPAL INVESTIGATOR: IAYARAM, MAKKUNI ADDRESS: UNIVERSITY OF TEXAS DEPT OF MICROBIOLOGY AUSTIN, TX 78712 PERFORMING ORG.: UNIVERSITY OF TEXAS AUSTIN, AUSTIN, TEXAS SPONSORING ORG.: NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES FY: 92 FUNDS: \$265,024

2/3/114 (Item 3 from file: 265)

0020434 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS

IDENTIFYING NO.: 9105934; 9105934 AGENCY CODE: NSF

Genetic Analysis of Pattern Formation During Drosophila Neurogenesis

PRINCIPAL INVESTIGATOR: Ellis, Hilary M Dr.

PERFORMING ORG.: Emory University, Biology, Atlanta, GA 30322

PROJECT MONITOR: Program Manager

SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY

& NEUROSCIENC, Washington, D.C., 20550

DATES: 910715 TO 920630 FY: 91 \ FUNDS: \$69,613

2/3/115 (Item 4 from file: 265)

0019890 PIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 9103946; 9103946 AGENCY CODE: NSF

Generation of Mosaicism in Mice by a Site-Specific Recombinase (FLP) PRINCIPAL INVESTIGATOR: 8 Gorman, Stephen Dr. PERFORMING ORG.: Salk Institute for Biological Studies, Gene Expression Laboratory, San Diego, CA 92128 PROJECT MONITOR: Thomas E. Brady SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY & NEUROSCIENC, Washington, D.C., 20550 DATES: 910315 TO 920831 FY: 91 FUNDS: \$49,522 2/3/116 (Item 5 from file: 265) 0016781 DIALOG\FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO : 9019220; 9019220 AGENCY CODE: NSF Genetic Analysis in Arabidopsis PRINCIPAL INVESTIGATOR: Signer, Ethan R Dr. ORG.: \ Massachusetts Institute of Technology, Biology, PERFORMING Cambridge, MA 02139 PROJECT MONITOR: DeLill Nasser SPONSORING ORG.: National Science Foundation, DIV OF MOLECULAR & CELLULAR BIOSCIENCES, Washington, D.C., 20550 DATES: 910201 TO 930731 FY 91 FUNDS: \$200,000 (Item 1 from file: 35) 2/3/117 01212062 ORDER NO: AADNN-59965 THE ROLE OF DNA BENDING IN FLP-MEDIATED SITE-SPECIFIC RECOMBINATION Author: SCHWARTZ, CAROL JUDITH ELAINE Degree: PH.D. Year: 1990 Corporate Source/Institution: UNIVERSITY OF TORONTO (CANADA) (0779) Source: VOLUME 52/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 5647. 209 PAGES 0-315-59965-0 ISBN: (Item 2 from file: 35) 2/3/118 01142876 ORDER NO: AAD90-30816 UNUSUAL DNA STRUCTURE IN SITE-SPECIFIC AND HOMOLOGOUS RECOMBINATION (RECOMBINATION) Author: UMLAUF, SCOTT W. Degree: PH.D. 1990 Years Corporate Source/Institution: THE UNIVERSITY OF WISCONSIN - MADISON (0262) Source: VOLUME 51/09-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 4199. 219 PAGES (Item 3 from file: 35) 2/3/119 1061565 ORDER NO: AAD89-12817 ANALYSIS OF THE MAJOR DNASE I HYPERSENSITIVE SITE ON THE YEAST TWO-MICRON DNA PLASMID Author: STRAND, ANDREW DAVID Degree: PH.D. Year: 1989 Corporate Source/Institution: UNIVERSITY OF MINNESOTA (0130) Source: VOLUME 50/02-B OF DISSERTATION ABSTRACTS INTERNATIONAL.

PAGE 446. 111 PAGES

2/3/120 (Item 4 from file: 35)

949308 ORDER NO: AAD87-06690

A GENETIC ANALYSIS OF FACTORS INVOLVED IN THE MAINTENANCE OF THE 2 MICRON PLASMID OF SACCHAROMYCES CEREVISIAE (CHROMATIN)

Author: VEIT, BRUCE EDWARD

Degree: PH.D. Year: 1986

Corporate Source/Institution: UNIVERSITY OF WASHINGTON (0250) Source: VOLUME 47/12-B OF DISSERTATION ABSTRACTS INTERNATIONAL.

PAGE 4763. 97 PAGES

2/3/121 (Item 1 from file: 51) 00405585 91-03-b0028 SUBFILE: FSTA

Yeast 2 MUm vectors replicate and undergo recombination in Torulaspora delbrueckii.

Compagno, C.; Ranzi, B. M.; Martegani, E.

Correspondence (Reprint) address, B. M. Ranzi, Dipartimento di Fisiologia e Biochimica Generali, Sezione di Biochimica Comparata, Univ. di Milano, Milan, Italy

Molecular Microbiology 1989 , 3 (8) 1003-1010 LANGUAGE: English

2/3/122 (Item 1 from file: 60)

09154644

PROJ NO: NYC-186301 AGENCY : SAES NY.C

PROJ TYPE: STATE

START: 01 JUL 91 TERM: 30 JUN 92

INVEST: MACINTYRE R J

ENTOMOLOGY

CORNELL UNIVERSITY

ITHACA NEW YORK 14853

DEVELOPMENT OF A MORE EFFICIENT INSECT TRANSFORMATION SYSTEM

OBJECTIVES: The goal of the research described below is to develop a system in which DNA canbe both easily and effectively delivered to insect embryos and, using the yeast "flip recombinase" system, insure the recovery of transgenic animals at high frequencies.

PRIMARY HEADINGS: R207 Insect Control-Field Crops; A4500 Protection Against Insects; C6500 Invertebrates; F1313 Physiology-Other

2/3/123 (Item 2 from file: 60)

09091400

PROJ NO: WIS02827 AGENCY : SAES WIS

PROJ TYPE: STATE

START: 01 JUL 86 TERM: 30 NOV 96

FY: 1989

INVEST: COX M M

BIOCHEMISTRY

UNIV OF WISCONSIN

MADISON WISCONSIN 53706

THE BIOCHEMISTRY OF GENETIC RECOMBINATION

OBJECTIVES: The FLP recombinase (derived from yeast) has been purified extensively. The properties of this protein and the recombination event it catalyzes are being studied in vitro. The recombination site utilized by this protein has been defined in detail. Studies on the mechanism of action of this recombination system are now getting underway.

PRIMARY HEADINGS: R318 Noncommodity Biotechnology, Biometry; A7000 Experimental Design, Statistical Methods; C6300 Biological Cell Systems; F0114 Biochemistry and Biophysics-Other

2/3/124 (Item 1 from file: 286)
0050984 Journal Announcement: 08APR91 Doc Type: 2
Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355

1ST COMPANY/ORGANIZATION NAME:
Salk Institute for Biological Studies, The, USA (1921)?

LOCUS YSCPLASM 6318 bp DNA circular PLN 31-JUL-1992 DEFINITION Yeast (S.cerevisiae) 2 micron circle plasmid, complete genome. ACCESSION J01347 L00321 L00322 L00323 L00324 M10185 M11111 M11593 M14239 M14240 M14241 M14242 M14243 M14244 M14245 M14253 M14254 M14255 M14256 M14257 M14258 M14259 M14591 M14592 M14593 M14594 M14595 M14596 M14597 M14598 V01323 KEYWORDS DNA-binding protein; Rep-1 protein; Rep-2 protein; circular; complete genome; d protein; plasmid; protein FLP; recombinase; repeat region. SOURCE Yeast (S.cerevisiae, strain A364A D5) DNA, clones pJDB71, p82-6B, CV20, pMMD2, pGP20, pJFS166 (see comment). ORGANISM Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Endomycetales; Saccharomycetaceae. REFERENCE 1 (bases 1 to 1022) AUTHORS Hindley, J. and Phear, G.A. TITLE Sequence of 1019 nucleotides encompassing one of the inverted repeats from the yeast 2 micron plasmid JOURNAL Nucleic Acids Res. 7, 361-375 (1979) MEDLINE 80034481 REFERENCE 2 (bases 1 to 6318; 1 to 6318) AUTHORS Hartley, J.L. and Donelson, J.E. TITLE Nucleotide sequence of the yeast plasmid JOURNAL Nature 286, 860-865 (1980) MEDLINE 81012161 REFERENCE 3 (bases 3891 to 3990) AUTHORS Broach, J.R., Guarascio, V.R. and Jayaram, M. TITLE Recombination within the yeast plasmid 2-micron circle is site-specific JOURNAL Cell 29, 227-234 (1982) MEDLINE 82259368 REFERENCE 4 (bases 3881 to 4020) AUTHORS McLeod, M., Volkert, F. and Broach, J.R. TITLE Components of the site-specific recombination system encoded by the veast plasmid 2-micron circle JOURNAL Cold Spring Harb. Symp. Quant. Biol. 49, 779-787 (1984) MEDLINE 85153059 REFERENCE 5 (bases 670 to 732) AUTHORS Andrews, B.J., Proteau, G.A., Beatty, L.G. and Sadowski, P.D. TITLE The FLP recombinase of the 2 micron circle DNA of yeast: Interaction with its target sequences JOURNAL Cell 40, 795-803 (1985) MEDLINE 85176933 REFERENCE 6 (bases 5570 to 5605) AUTHORS Babineau, D., Vetter, D., Andrews, B.J., Gronostajski, R.M., Proteau, G.A., Beatty, L.G. and Sadowski, P.D. TITLE The FLP protein of the 2-micron plasmid of yeast: Purification of the protein from Escherichia coli cells expressing the cloned FLP JOURNAL J. Biol. Chem. 260, 12313-12319 (1985) MEDLINE 86008307 REFERENCE 7 (sites) AUTHORS Gronostajski, R.M. and Sadowski, P.D. TITLE Determination of DNA sequences essential for FLP-mediated recombination by a novel method JOURNAL J. Biol. Chem. 260, 12320-12327 (1985) MEDLINE 86008308

OOK DNA? 80 ASS

QH301. CC

REFERENCE 8 (sites)

AUTHORS Sutton, A. and Broach, J.R.

TITLE Signals for transcription initiation and termination in the Saccharomyces cerevisiae plasmid 2 micron circle

JOURNAL Mol. Cell. Biol. 5, 2770-2780 (1985)

MEDLINE 86284639

REFERENCE 9 (sites)

AUTHORS Gronostajski, R.M. and Sadowski, P.D.

TITLE The FLP recombinase of the Saccharomyces cerevisiae 2-micron plasmid attaches covalently to DNA via a phosphotyrosyl linkage

JOURNAL Mol. Cell. Biol. 5, 3274-3279 (1985)

MEDLINE 86310798

REFERENCE 10 (bases 667 to 739)

AUTHORS Senecoff, J.F., Bruckner, R.C. and Cox, M.M.

TITLE The FLP recombinase of the yeast 2-micron-m plasmid: Characterization of its recombination site

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82, 7270-7274 (1985)

MEDLINE 86042647

REFERENCE 11 (sites)

AUTHORS McLeod, M., Craft, S. and Broach, J.R.

TITLE Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 micron circle

JOURNAL Mol. Cell. Biol. 6, 3357-3367 (1986)

MEDLINE 87089667

COMMENT [8] sites; mRNA CAP sites and poly-adenylation sites. [9] sites; FLP binding.

[7] sites; FLP cleavage.

[11] sites; FLP-mediated recombination crossover site. Draft entry and clean copy sequence for [5] kindly provided by J.Senecoff, 24-JAN-1986.

Yeast 2 micron plasmid contains two 599 bp inverted repeats separated by a large unique (UL) and a small unique (US) region. During recombination the UL and US regions invert producing two sequence forms that differ in the orientation of one unique region relative to the other. The A form is presented below. FLP is the only 2-micron circle-encoded protein needed for specific site recombination between the IRs of 2-micron circle. The minimal size of the recombination site required for efficient FLP recombinase-catalyzed recombination in vitro is no more than 28 bp, which includes parts of two 13 bp inverted repeats (positions 690-702 and 711-723) and all of an 8 bp spacer (703-710) [5]. The FLP recombinase cleaves the DNA at the boundaries of the spacer and becomes covalently linked to the spacer DNA [5],[9]. The efficiency of the recombination is reduced if the spacer in a recombinant site is increased or decreased by 1 bp. while the spacer in the second site is unaltered [5]. Recombination between two sites with identical 1-base pair additions or deletions is relatively unaffected, suggesting that pairing of sequences in the spacer regions is important in FLP-promoted recombination events [5]. The sequence asymmetry utilized by the recombinase to determine the orientation of the site is located uniquely within the spacer region. Another 13 bp direct repeat, is found at positions 676-688 [5]. FLP-mediated recombination involving two FLP sites that are inverted with respect to each other results in inversion of the DNA sequences between the sites [4]. If the participating recombination sites are in direct orientation, FLP

A start codon in phase with the Rep1 coding region is located at positions 1966-1964. Two CAP sites for Rep1 mRNA are located beyond the 'atg' codon (position 2008) at positions 2004 and 2005. Complete source information: Yeast (S.cerevisiae, strain A364A D5) DNA, clones pJDB71 [1], p82-6B [2], CV20 [3], pMMD2 [4], pGP20 [5], pJFS166 [10]. NCBI gi: 172190 **FEATURES** Location/Qualifiers 1..6318 source /organism="Saccharomyces cerevisiae" 1..545 exon conflict replace((157.160)..(157.160),**) /citation=[1] replace((289.290)..(289.290),"") conflict /citation=[1] repeat_region 341..939 /note="IR2" replace((464.466)..(464.466),"") conflict /citation=[1] replace(558,"") conflict /citation=[1] conflict replace(561,"") /citation=[1] conflict replace((622.624)..(622.624),**) /citation=[1] replace(642,"") conflict /citation=[1] conflict replace((665.666)..(665.666),"") /citation=[1] misc_binding 673..722 /note="FLP recombinase binding site A [9]" /bound_moiety="FLP recombinase" conflict replace((793.794)..(793.794),") /citation=[1] complement(836..2038) mRNA /note="Rep1 mRNA (alt.)" mRNA complement(836..2017) /note="Rep1 mRNA (alt.)" complement(836..2019) mRNA /note="Rep1 mRNA (alt.)" complement(836..2010) mRNA /note="Rep1 mRNA (alt.)" mRNA complement(836..2004) /note="Rep1 mRNA (alt.)" mRNA complement(836..2005) /note="Rep1 mRNA (alt.)" CDS complement(887..2008) /note="Rep 1 protein; NCBI gi: 172192" /codon_start=1 /db_xref="PID:g172192" /translation="MNGERLLACIKQCIMQHFQPMVYDESRCVIETTRGTFPVPDNYK KYKTLAFAFVGHVLNTDDTPVIEKELDWPDPALVYNTIVDRIINHPELSQFISVAFIS QLKATIGEGLDINVKGTLNRRGKGIRRPKGVFFRYMESPFVNTKVTAFFSYLRDYNKI

promotes only the excision of the intervening DNA sequences [4]. The Rep 1 and Rep proteins are involved plasmid partitioning and

protein stability.

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ELPPEEDPSRELNNVQHEVNSLTEQDAEADEGLWGEIDSLCEKWQSEAEDQTEAEIIA
        DRIIGNSQRMANLKIRRTKFKSVLYHILKELIQSQGTVKVYRGSSFSHDSIKISLHYE
        EQHITAVWYLTVKFEEHWKPVDVEVEFRCKFKERKVDG"
mRNA
           2254..2841
        /note="D mRNA (alt.; 5' end +/- 3 bp)"
mRNA
           2254..2861
        /note="D mRNA (alt.; 5' end +/- 3 bp)"
CDS
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        /codon_start=1
        /db_xref="PID:g172193"
        /translation="MPYKTAIDCIEELATQCFLSKLTDDDVSTFRRVCSKENDIIKLA
        LRIPRTIDYTSILRLLYDTLPLRSLSFNEALPLFCYSIDPAQQRQCDLRFYLRDVVKL
        ARPRKRLEMQKALLQWLPSLLSDVTLQLLNDIRIRFEEIQPNIRQTVLQIYDRTCYPS
        LNFEHPNLGVFPETDSIFEPV*
repeat_region 3714..4312
        /note="IR1"
misc_binding 3930..3979
        /note="FLP-recombinase binding site B [9]"
        /bound_moiety="FLP recombinase"
mRNA
           complement(4108..5182)
        /note="REP2 mRNA (major alt.)"
           complement(4108..5183)
mRNA
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mRNA
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mRNA
        /note="REP2 mRNA (major alt.)"
           complement(4108..5198)
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mRNA
           complement(4108..5196)
        /note="REP2 mRNA (major alt.)"
           complement(4108..5197)
mRNA
        /note="REP2 mRNA (major alt.)"
           complement(4108..5212)
mRNA
        /note="REP2 mRNA (minor alt.)"
CDS
          complement(4308..5198)
        /note="Rep 2 protein; NCBI gi: 172194"
        /codon_start=1
        /db_xref="PID:g172194"
        /translation="MDDiETAKNLTVKARTAYSVWDVCRLFIEMIAPDVDIDIESKRK
        SDELLFPGYVIRPMESLTTGRPYGLDSSAEDSSVSSDSSAEVILPAAKMVKERFDSIG
        NGMLSSQEASQAAIDLMLQNNKLLDNRKQLYKSIAIIIGRLPEKDKKRATEMLMRKMD
        CTQLLVPPAPTEEDVMKLVSVVTQLLTLVPPDRQAALIGDLFIPESLKDIFNSFNELA
        AENRLQQKKSELEGRTEVNHANTNEEVPSRRTRSRDTNARGAYKLQNTITEGPKAVPT
        KKRRVATRVRGRKSRNTSRV*
mRNA
           join(5549..6318,1..545)
        /note="Flp mRNA"
          5549..6318
exon
          join(5570..6318,1..523)
CDS
        /note="recombinase (FLP); NCBI gi: 172191"
        /codon_start=1
       /db_xref="PID:g172191"
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/translation="MPQFGILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWM"

ASEYHNNTKFILTFSCQAYWASGPNFSALKNVIRCSIIHEYISKFVEREQDKGHIGDQ

ITHNGTAIKRATFMSYNTIISNSLSFDIVNKSLQFKYKTQKATILEASLKKLIPAWEF
TIIPYYGQKHQSDITDIVSSLQLQFESSEEADKGNSHSKKMLKALLSEGESIWEITEK
ILNSFEYTSRFTKTKTLYQFLFLATFINCGRFSDIKNVDPKSFKLVQNKYLGVIIQCL
VTETKTSVSRHIYFFSARGRIDPLVYLDEFLRNSEPVLKRVNRTGNSSSNKQEYQLLK
DNLVRSYNKALKKNAPYSIFAIKNGPKSHIGRHLMTSFLSMKGLTELTNVVGNWSDKR
ASAVARTTYTHQITAIPDHYFALVSRYYAYDPISKEMIALKDETNPIEEWQHIEQLKG
SAEGSIRYPAWNGIISQEVLDYLSSYINRRI'

old_sequence replace(5583,**)

/citation=[2]

BASE COUNT 1876 a 1284 c 1179 g 1979 t

ORIGIN 1 bp upstream of EcoRI site.

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- 61 ggaataccaa ttattaaaag ataacttagt cagatcgtac aataaagctt tgaagaaaaa
- 121 tgcgccttat tcaatctttg ctataaaaaa tggcccaaaa tctcacattg gaagacattt
- 181 gatgacctca tttctttcaa tgaagggcct aacggagttg actaatgttg tgggaaattg
- 241 gagogataag ogtgottotg oogtggooag gacaacgtat actoatcaga taacagcaat
- 301 acctgateae taettegeae tagttteteg gtaetatgea tatgateeaa tateaaagga
- 361 aatgatagca ttgaaggatg agactaatcc aattgaggag tggcagcata tagaacagct
- 421 aaagggtagt getgaaggaa geataegata eeeegeatgg aatgggataa tateacagga
- 481 ggtactagac tacctttcat cctacataaa tagacgcata taagtacgca tttaagcata
- 541 aacacgcact atgccgttct tctcatgtat atatatatac aggcaacacg cagatatagg
- 601 tgcgacgtga acagtgagct gtatgtgcgc agctcgcgtt gcattttcgg aagcgctcgt
- 661 tttcggaaac gctttgaagt tcctattccg aagttcctat tctctagaaa gtataggaac
- 721 ttcagagege ttttgaaaac caaaageget etgaagaege aetttcaaaa aaccaaaaac
- 781 gcaccggact gtaacgagct actaaaatat tgcgaatacc gcttccacaa acattgctca
- 841 aaagtatete titigetatat atetetgige tatateeeta tataaeetae eeateeaeet
- 901 ttegeteett gaacttgeat etaaactega eetetacate aacaggette caatgetett
- 961 caaattttac tgtcaagtag acccatacgg ctgtaatatg ctgctcttca taatgtaagc
- 1021 ttatctttat cgaatcgtgt gaaaaactac taccgcgata aacctttacg gttccctgag
- 1081 attgaattag tteetttagt atatgataea agaeaetttt gaaetttgta egaegaattt
- 1141 tgaggttege catectetgg ctattteeaa ttateetgte ggetattate teegeeteag
- 1201 tttgatette egetteagae tgeeattttt eacataatga atetatttea eeceacaate
- 1261 cttcatcege etcegeatet tgtteegtta aactattgae tteatgttgt acattgttta
- 1321 gttcacgaga agggtcctct tcaggcggta gctcctgatc tcctatatga cctttatcct
- 1381 gttctctttc cacaaactta gaaatgtatt catgaattat ggagcaccta ataacattct
- 1441 tcaaggcgga gaagtttggg ccagatgccc aatatgcttg acatgaaaac gtgagaatga
- 1501 atttagtatt attgtgatat tctgaggcaa ttttattata atctcgaaga taagagaaga
- 1561 atgcagtgac ctttgtattg acaaatggag attccatgta tctaaaaaat acgcctttag
- 1621 gocttctgat accctttccc ctgcggttta gcgtgccttt tacattaata tctaaaccct
- 1681 ctccgatggt ggcctttaac tgactaataa atgcaaccga tataaactgt gataattctg
- 1741 ggtgatttat gattcgatcg acaattgtat tgtacactag tgcaggatca ggccaatcca
- 1801 gttctttttc aattaccggt gtgtcgtctg tattcagtac atgtccaaca aatgcaaatg
- 1861 ctaacgtttt gtattictta taattgtcag gaactggaaa agtccccctt gtcgtctcga
- 1921 ttacacacct actticateg tacaccatag gitggaagig etgeataata cattgettaa
- 1981 tacaagcaag cagtototog coattoatat ttoagttatt ttocattaca gotgatgtoa
- 2041 ttgtatatca gegetgtaaa aatetatetg ttacagaagg ttttegeggt ttttataaac
- 2101 aaaactttog ttacgaaatc gagcaatcac cccagctgcg tatttggaaa ttcgggaaaa
- 2161 agtagageaa egegagttge attitttaca ecataatgea tgattaaett egagaaggga
- 2221 ttaaggctaa tttcactagt atgtttcaaa aacctcaatc tgtccattga atgccttata
- 2281 aaacagctat agattgcata gaagagttag ctactcaatg ctttttgtca aagcttactg
- 2341 atgatgatgt gtctactttc aggegggtct gtagtaagga gaatgacatt ataaagctgg
- 2401 cacttagaat tocacggact atagactata ctagtatact cogtotactg tacgatacac
- 2461 ttccgctcag gtccttgtcc tttaacgagg ccttaccact cttttgttac tctattgatc
- 2521 cageteagea aaggeagtgt gatetaagat tetatetteg egatgtagta aaactageta
- 2581 gaccgagaaa gagactagaa atgcaaaagg cacttctaca atggctgcca tcattattat
- 2641 cogatgigac gotgoagott otoaatgata tiogaatacg ottigaggag atacagoota
- 2701 atateegaca aactgtttta cagatttaeg ategtaettg ttaceeatea ttgaattttg

2761 aacatccgaa cctgggagtt ttccctgaaa cagatagtat atttgaacct gtataataat 2821 atatagtota gegetttaeg gaagacaatg tatgtattte ggtteetgga gaaactattg 2881 catctattgc ataggtaatc ttgcacgtcg catccccggt tcattttctg cgtttccatc 2941 ttgcactica atagcatatc tttgttaacg aagcatctgt gcttcatttt gtagaacaaa 3001 aatgcaacgc gagagcgcta atttttcaaa caaagaatct gagctgcatt tttacagaac 3061 agaaatgcaa cgcgaaagcg ctattttacc aacgaagaat ctgtgcttca tttttgtaaa 3121 acaaaaatgc aacgcgagag cgctaatttt tcaaacaaag aatctgagct gcatttttac 3181 agaacagaaa tgcaacgcga gagcgctatt ttaccaacaa agaatctata cttctttttt 3241 gttctacaaa aatgcatccc gagagcgcta tttttctaac aaagcatctt agattacttt 3301 ttttctcctt tgtgcgctct ataatgcagt ctcttgataa ctttttgcac tgtaggtccg 3361 ttaaggttag aagaaggeta etttggtgte tattttetet teeataaaaa aageetgaet 3421 ccacttcccg cgtttactga ttactagcga agctgcgggt gcatttttc aagataaagg 3481 catccccgat tatattctat accgatgtgg attgcgcata ctttgtgaac agaaagtgat 3541 agcgttgatg attetteatt ggteagaaaa ttatgaaegg tttettetat tttgteteta 3601 tatactacgt ataggaaatg tttacatttt cgtattgttt tcgattcact ctatgaatag 3661 ttcttactac aatttttttg totaaagagt aatactagag ataaacataa aaaatgtaga 3721 ggtcgagttt agatgcaagt tcaaggagcg aaaggtggat gggtaggtta tatagggata 3781 tagcacagag atatatagca aagagatact tttgagcaat gtttgtggaa gcggtattcg 3841 caatatttta gtagctcgtt acagtccggt gcgtttttgg ttttttgaaa gtgcgtcttc 3901 agagegettt tggttttcaa aagegetetg aagtteetat aetttetaga gaataggaac 3961 ttcggaatag gaacttcaaa gcgtttccga aaacgagcgc ttccgaaaat gcaacgcgag 4021 ctgcgcacat acagctcact gttcacgtcg cacctatatc tgcgtgttgc ctgtatatat 4081 atatacatga gaagaacggc atagtgcgtg tttatgctta aatgcgtact tatatgcgtc 4141 tatttatgta ggatgaaagg tagtctagta cctcctgtga tattatccca ttccatgcgg 4201 ggtategtat getteettea geactaceet ttagetgtte tatatgetge eacteeteaa 4261 ttggattagt ctcatccttc aatgctatca tttcctttga tattggatca taccctagaa 4321 gtattacgtg attttctgcc ccttaccctc gttgctactc tccttttttt cgtgggaacc 4381 gctttagggc cctcagtgat ggtgttttgt aatttatatg ctcctcttgc atttgtgtct 4441 ctacttcttg ttcgcctgga gggaacttct tcatttgtat tagcatggtt cacttcagtc 4501 cttocttoca actoactott tttttgotgt aaacgattot otgoogooag ttoattgaaa 4561 ctattgaata tatcctttag agattccggg atgaataaat cacctattaa agcagcttga 4621 cgatctggtg gaactaaagt aagcaattgg gtaacgacgc ttacgagctt cataacatct 4681 tetteegttg gagetggtgg gaetaataac tgtgtacaat ceattttet eatgageatt 4741 toggtagete tettettgte ttteteggge aatetteeta ttattatage aatagatttg 4801 tatagttgct ttctattgtc taacagcttg ttattctgta gcatcaaatc tatggcagcc 4861 tgacttgctt cttgtgaaga gagcatacca tttccaatcg aatcaaacct ttccttaacc 4921 atcttegeag caggeaaaat taccteagea etggagteag aagataeget ggaatettet 4981 gogotagaat caagaccata oggootacog gttgtgagag attocatggg cottatgaca 5041 tateetggaa agagtagete ateagaetta egittaetet etatateaat atetaeatea 5101 ggagcaatca tttcaataaa cagccgacat acatcccaga cgctataagc tgtacgtgct 5161 tttaccgtca gattcttggc tgtttcaatg tcgtccattt tggttttctt ttaccagtat 5221 tgttcgtttg ataatgtatt cttgcttatt acattataaa atctgtgcag atcacatgtc 5281 aaaacaactt tttatcacaa gatagtaceg caaaacgaac etgegggeeg tetaaaaatt 5341 aaggaaaagc agcaaaggtg catttttaaa atatgaaatg aagataccgc agtaccaatt 5401 attitogoag tacaaataat gogoggoogg tgoattitto gaaagaacgo gagacaaaca 5461 ggacaattaa agttagtttt togagttago gtgtttgaat actgcaagat acaagataaa 5521 tagagtagtt gaaactagat atcaattgca cacaagatcg gcgctaagca tgccacaatt 5581 tggtatatta tgtaaaacac cacctaaggt gettgttegt eagtttgtgg aaaggtttga 5641 aagacettea ggtgagaaaa tageattatg tgetgetgaa etaacetatt tatgttggat 5701 gattacacat aacggaacag caatcaagag agccacattc atgagctata atactatcat 5761 aagcaattog otgagtttog atattgtoaa taaatcacto cagtttaaat acaagacgoa 5821 aaaagcaaca attotggaag ootoattaaa gaaattgatt ootgottggg aatttacaat 5881 tattocttac tatggacaaa aacatcaatc tgatatcact gatattgtaa gtagtttgca 5941 attacagttc gaatcatcgg aagaagcaga taagggaaat agccacagta aaaaaatgct 6001 taaagcactt ctaagtgagg gtgaaagcat ctgggagatc actgagaaaa tactaaattc 6061 attigagtat acticgagat ttacaaaaac aaaaacttta taccaattoc tottoctago 6121 tactttcatc aattgtggaa gattcagcga tattaagaac gttgatccga aatcatttaa

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